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**Get Subsequence****1: AAA28373. Antennepedia prot...[gi:156934]**

BLink, Domains, Links

LOCUS AAA28373 74 aa linear INV 26-APR-1993
DEFINITION Antennepedia protein.
ACCESSION AAA28373
VERSION AAA28373.1 GI:156934
DBSOURCE locus DROANTC2 accession K01948.1
KEYWORDS
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 .(residues 1 to 74)
AUTHORS McGinnis,W., Garber,R.L., Wirz,J., Kuroiwa,A. and Gehring,W.J.
TITLE A homologous protein-coding sequence in Drosophila homeotic genes
and its conservation in other metazoans
JOURNAL Cell 37 (2), 403-408 (1984)
MEDLINE 84205674
PUBMED 6327065
COMMENT Method: conceptual translation.
FEATURES Location/Qualifiers
source 1..74
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/map="right arm of ch. 3"
Protein 1..74
/name="Antennepedia protein"
CDS 1..74
/coded_by="complement(K01948.1:<1..>222)"
ORIGIN
1 iylepterkr grqtytryqt lelekefhfn ryltrrrrie iahalciter qikiwfqnrr
61 mwkkenktk gepd
//

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>gi|156934|gb|AAA28373.1| Antennepedia protein
Length = 74

Score = 61.7 bits (138), Expect = 1e-09
Identities = 16/16 (100%), Positives = 16/16 (100%)

Query: 1 RQIKIWFQNRRMKWKK 16
RQIKIWFQNRRMKWKK
Sbjct: 50 RQIKIWFQNRRMKWKK 65

 NCBI	BLAST	Protein	Structure	PubMed	Taxonomy
	Genome	Nucleotide	3D-Domains	Books	Help

Query: gi|156934 Antennepedia protein

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200 BLAST hits to 59 unique species [Sort by taxonomy proximity](#)

 Archaea  Bacteria  Metazoa  Fungi  Plants  Viruses  Other Eukaryotae

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74 aa

	SCORE	P	ACCESSION	GI	PROTEIN DESCRIPTION
	362	20	AAC31945	3420836	Antennapedia homeotic protein [Anop
	362	19	BAA04087	391615	Antennapedia homologue protein [Bom
	362	35	A25399	84890	homeotic protein Antennapedia - fru
	362	34	AAO00997	27374237	Antp-PA [Drosophila erecta]
	362	20	EAA07256	21295111	agCP12956 [Anopheles gambiae str. P
	362	19	S58850	1363994	homeotic protein abd-A - Junonia co
	362	32	CAA43307	829192	Antp [Drosophila subobscura]
	357	31	AAA28737	158023	homeobox protein
	357	35	1HOM	443020	Chain , Antennapedia Protein (Home
	355	19	AAF69136	7767519	prothoraxless [Tribolium castaneum]
	355	19	AAK96031	15450324	homeodomain transcription factor Pr
	349	19	CAC06383	9967824	Antennapedia protein [Apis mellifer

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	198	100.0	2100	6 AX12124	AX412124 Sequence	
2	194.8	98.4	2691	6 AR16400	AR116702 Sequence	
3	194.8	98.4	2691	6 AR116702	AR116702 Sequence	
4	194.8	98.4	2691	10 MU88990	U88990 Mus musculus	
5	186.8	94.3	1988	10 MU036842	U36842 Mus musculus	
6	182	91.9	1491	10 AF183429	AF183429 Rattus norvegicus	
7	182	91.9	2458	10 AR033366	AB033366 Rattus norvegicus	
8	182	91.9	2032	10 AF304334	AF304334 Rattus norvegicus	
9	180.4	91.1	2032	10 AF043334	AF304334 Rattus norvegicus	
10	173	87.4	1659	6 E31042	E31042 Method for	
11	173	87.4	1659	9 U32974	U32974 Human IAP-1	
12	173	87.4	2086	9 BC032729	BC032729 Homo sapiens	
13	173	87.4	2404	6 AX429575	AX429575 Sequence	
14	173	87.4	2540	6 AR103281	AR103281 Sequence	
15	173	87.4	2540	6 AX12118	AX412118 Sequence	
16	173	87.4	2540	9 U45880	U45880 Human X-11n	
17	173	87.4	3000	6 AX412111	AX412111 Sequence	
18	173	87.4	5232	6 AR106397	AR106397 Sequence	
19	173	87.4	5232	6 AR116699	AR116699 Sequence	
20	157	79.3	1752	6 AX104956	AX104956 Sequence	
21	157	79.3	1752	9 AF164681	AF164681 Homo sapiens	
22	157	79.3	154214	9 AC079753	AC079753 Homo sapiens	
23	149	75.3	1758	6 AX370787	AX370787 Sequence	
24	149	75.3	1758	6 AX370789	AX370789 Sequence	
25	149	75.3	4993	6 AX104968	AX104968 Sequence	
26	149	75.3	4993	9 AF164682	AF164682 Homo sapiens	
C	27	149	75.3	144301	9 AC010467	AC010467 Homo sapiens
C	28	149	75.3	165662	9 AC092070	AC092070 Homo sapiens
C	29	147.4	74.4	711	6 AR121220	AR121220 Sequence
C	30	147.4	74.4	711	6 AR123871	AR123871 Sequence
C	31	147.4	74.4	2032	9 AF120440	AF120440 Homo sapiens
C	32	145.8	73.6	711	6 AX104970	AX104970 Sequence
C	33	145.8	73.6	711	9 AT030052	AT030052 Pan troglodytes
C	34	144.2	72.8	711	6 AX104972	AX104972 Sequence
C	35	144.2	72.8	711	9 AV030053	AV030053 Gorilla gorilla
C	36	131.6	66.5	187568	9 AP002967	AP002967 Homo sapiens
C	37	130	65.1	184439	2 AP003085	AP003085 Homo sapiens
C	38	121.4	61.3	327	4 AF428770	AF458770 Bos taurus
C	39	104.2	52.6	1740	5 AF451854	AF451854 Gallus gallus
C	40	85.8	43.3	133391	9 HSD315G1	AL121601 Human DNA
C	41	85.8	43.3	201197	2 HS424J12	282207 Homo sapiens
C	42	77	38.9	1550	4 SSU9142	U79142 Sus scrofa
C	43	76.6	38.7	158093	9 AL390123 Human DNA	
C	44	76	38.4	2563	9 HUMSCPB	L49432 Homo sapiens
C	45	76	38.4	2601	6 AR129833	AR129833 Sequence

ALIGNMENTS

RESULT 1	AX412124	LOCUS Sequence 224 from Patent WO022996B.	DNA	linear	PAT 15-JUN-2002
DEFINITION	AX412124	ACCESSION AX412124			
KEYWORDS	AX412124.1	VERSION GI:21444584			
SOURCE	house mouse.				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.				
AUTHORS	Antisense IAP nucleic acids and uses thereof				
TITLE	Patent: WO 026568-A 22 04-APR-2002;				
JOURNAL					

Pre. No. is the number of results predicted by chance to have a

FEATURES University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)
 SOURCE 1..2100
 /organism="Mus musculus"
 /db_xref="taxon:10030"
 BASE COUNT 615 a -417 c 482 g 586 t
 ORIGIN

Query Match 100.0%; Score 198; DB 6; Length 2100;
 Best Local Similarity 100.0%; Pred. No. 7.1e-46;
 Matches 198; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0;

Qy 1 TATGAGCAGGATCGTTACATTGGAACATGGATACTACTAGTTAACAGGAGCTT 60
 Db 916 TTGAAACCAACGATCGTTACATTGGAACATGGATACTACTAGTTAACAGGAGCTT 975
 Qy 61 GGAGAGCTGGATTATGCTTAGGTGAAGGGATAAAGGGAATGCTCACTGTGGA 120
 Db 976 GCAAGACTCTGGATTATGCTTAGGTGAAGGGATAAAGGGAATGCTCACTGTGGA 1035
 Qy 121 GGAGGGCTCACGGATTGCAAGTGAAGGCAACTGGACCAGCATGCTAC 180
 Db 1036 GGAGGGCTCACGGATTGCAAGTGAAGGCAACTGGACCCTGGGACAGATGCTAAGTGCTAC 1095
 Qy 181 CCAGGGTGCATAATACCTA 198
 Db 1096 CCAGGGTGCATAATACCTA 1113

RESULT 2
 AR106400
 LOCUS AR106400
 DEFINITION Sequence 9 from patent US 6107041.
 ACCESSION AR106400
 VERSION GI:12820930
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2691)
 AUTHORS Korneluk,R.G., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.
 TITLE Detection and modulation of IAPS for the diagnosis and treatment of proliferative disease
 JOURNAL Patent: US 6107041-A 9 22-AUG-2000;
 FEATURES Location/Qualifiers 1..2691
 BASE COUNT 819 a -479 c 562 g 831 t
 ORIGIN

Query Match 98.4%; Score 194.8; DB 6; Length 2691;
 Best Local Similarity 99.0%; Pred. No. 5.5e-45;
 Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TATGAGCAGGATCGTTACATTGGAACATGGATACTACTAGTTAACAGGAGCTT 60
 Db 1461 TTGAAACCAACGATCGTTACATTGGAACATGGATACTACTAGTTAACAGGAGCTT 1520
 Qy 61 GGAGAGCTGGATTATGCTTAGGTGAAGGGATAAAGGGAATGCTCACTGTGGA 120
 Db 1521 GCAAGAGCTGGATTATGCTTAGGTGAAGGGATAAAGGGAATGCTCACTGTGGA 1580
 Qy 121 GGAGGGCTCACGGATTGGAAGGCCAASTGAAGGCCCTGGGACAGATGCTAAGTGCTAC 180
 Db 1581 GGAGGGCTCACGGATTGGAAGGCCAAATGTAAGGCTCAAGGGAATGCTCACTGTGGA 1640

RESULT 4
 MMU88930
 LOCUS MMU88930
 DEFINITION Mus musculus x-linked inhibitor of apoptosis (miap-3) mRNA,
 complete cds.
 ACCESSION U88930
 VERSION U88930.1 GI:2138318
 KEYWORDS Unknown.
 SOURCE Mus musculus.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 2691)
 AUTHORS Farahani,R., Lefebvre,C., Korneluk,R.G. and MacKenzie,R.E.
 TITLE Genomic Organization and Primary Characterization of miap-3: The Murine Homologue of Human X-linked IAP
 JOURNAL Unpublished
 FEATURES Source
 BASE COUNT 2 (bases 1 to 2691)
 ORIGIN
 JOURNAL Direct Submission
 FEATURES Submitted (07-FEB-1997) Molécular Genetics, Children's Hospital of Eastern Ontario, 401 Smyth Rd., Ottawa, Ontario K1H 8L1, Canada
 SOURCE 1..2691
 /organism="Mus musculus"
 /db_xref="Taxon:10090"
 /chromosome="X"
 /map="P3-A5 region"
 /dev_stage="embryo"
 /gene="miap-3"
 / exon <1..1545

/gene="mimap-3"		JOURNAL PROC. NATL. ACAD. SCI. U.S.A. 93 (10), 4974-4978 (1996)
/number=1		JOURNAL MEDLINE 96209843 PUBMED 8643514
672. 2162		REFERENCE 2 (bases 1 to 1988)
/gene="mimap-3"		AUTHORS Vaux, D.L., Uren, A.G. and Pakusch, M.
/codon_start=1		TITLE Direct Submission
/product="X-linked inhibitor of apoptosis"		JOURNAL Submitted (21-SEP-1995) M. Pakusch, The Walter and Eliza Hall Institute, Royal Parade, Parkville, Victoria 3050, Australia
/protein_id="AAB58376.1"		LOCATION/Qualifiers
/db_xref="GI: 2138319"		1. 1988
/translation="MFTNSFQGTRTFLVDAFDNKEEVEFNRLKTFANFPSSPVSA		/organism="Mus musculus"
STLARGFLYTGIVDQFCGCHAAIDRWQYGDASGRHRISPCNRCFINGFYFENGAA		/strain="C57 Black 6 x CBA"
AQSTNCNGCQXKSENCGYGRNPFPDFRPPETHADYLILRGQYDQVQTCGGGLKNNPFPDRAWS		/db_xref="Taxon:10090"
CSEEARLKSFRNPWDFIAHLTRELASAGLYTGADQQVTCGGGLKNNPFPDRAWS		/sex="female"
EHRHFPNCFVFLGRVNRVRESGISDRNPNSTSIPRNPAAMEYARIVTFGTWTS		/tissue_type="liver"
SYNEKOOLARAGEYALGEGDVKYCFCIGGGLTDWKISSEPDNDQHACYPGCKYLLDEKG		/dev_stage="6-8 weeks old"
QEYINNHTLPLRFLESLSLEYLIAUDVSAQDNTEDESSOSLQD1STEQLRQLKEKLKTM		1. 1988
ICMDRNTAIVYFPCGHLCATCKOCAEAIVDKCPMCYTIVTFNOKIWS"		/gene="MIHA"
1546. 1645		212. 1702
/gene="mimap-3"		/gene="MIHA"
/number=2		/note="apoptosis inhibitor; homolog of Baculovirus IAP protein"
1646. 1724		/codon_start=1
/gene="mimap-3"		/product="MIHA"
/number=3		/protein_id="AAC52594.1"
1725. 1767		/db_xref="GI: 11452261"
/gene="mimap-3"		/translation="MFVNFSEGTRTEWLADNPKDEEEVEENPLRTFANEFSSSPVSA
/number=4		STLARAFLYTGEGDIDQCFCSHAIDRWQYGDASGRHRISPCNRCFINGFYFENGAA
1768. 1768		AOSTNPQNGQKSENCGYGRNPFPDFRPPETHADYLILRGQYDQVQTCGGGLKNNPFPDRAWS
/gene="mimap-3"		CSEEARLKSFRNPWDFIAHLTRELASAGLYTGADQQVTCGGGLKNNPFPDRAWS
/number=5		EHRHFPNCFVFLGRVNRVRESGISDRNPNSTSIPRNPAAMEYARIVTFGTWTS
1969. >2691		SYNEKOOLARAGEYALGEGDVKYCFCIGGGLTDWKISSEPDNDQHACYPGCKYLLDEKG
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/number=6		EERIKQTSGSSYSLTLESLVLEIADVSAQDNTEDESSOSLQD1STEQLRQLKEKLKTM
BASE COUNT 819 a 479 c 562 g 831 t		ICMDRNTAIVYFPCGHLCATCKOCAEAIVDKCPMCYTIVTFNOKIWS"
ORIGIN		287. 490
Query Match 98.4%	Score 194.8;	/gene="MIHA"
Best Local Similarity 99.0%	Pred. No. 5.5e-45;	/note="BIR repeat 1"
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		698. .901
		/gene="MIHA"
Qy 1 TATGAAGCCAGGATCGTTACTCTTGGAAACATGGATAATCTCAGTTAACAGGAGCAGCTT 60		/note="BIR repeat 2"
Db 1461 TATGAAGCACGGATCGTTACTCTTGGAAACATGGATAATCTCAGTTAACAGGAGCAGCTT 1520		1001. 1198
		/gene="MIHA"
Qy 61 CCAGAGCTGGATTTTATGCTTTAGTGAAAGCGATAAAGTAAGCTCTTCACTGTGGA 120		/note="BIR repeat 3"
Db 1521 CCAGAGCTGGATTTTATGCTTTAGTGAAAGCGATAAAGTAAGCTCTTCACTGTGGA 1580		1556. 1660
		/gene="MIHA"
Qy 121 GGAGGGCTCACGGATGGAAAGCCAAGTGAAGACCCCTGGGACAGCATGTGCTAC 180		/note="RING finger"
Db 1581 GGAGGGCTCACGGATGGAAAGCCAAGTGAAGACCCCTGGGACAGCATGTGCTAC 1640		367 c 459 g 557 t
		BASE COUNT 605 a
ORIGIN		94.3% Score 186.8; Best Local Similarity 96.5%; Length 1988;
		Matches 191; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
		1 TATGAAGCACGGATCGTTACTCTTGGAAACATGGATAATCTCAGTTAACAGGAGCAGCTT 60
		Db 1001 TATGAAGCACGGATCGTTACTCTTGGAAACATGGACAATCTCAGTTAACAGGAGCAGCTT 1060
		Qy 61 CCAGAGCTGGATTTTATGCTTTAGTGAAAGCGATAAAGTAAGCTCTTCACTGTGGA 120
		Db 1121 GGAGGGCTCACGGATGGAAAGCCAAGTGAAGACCCCTGGGACAGCATGTGCTAC 1180
		Db 1061 GCAGAGCTGGATTTTATGCTTTAGTGAAAGCGATAAAGTAAGCTCTTCACTGTGGA 1120
RESULT 5 MN06842	MNU36842	Qy 1181 CCAGGGTGCATAACTCA 198
LOCUS	Mus musculus IAP homolog A (MIHA)	Db 1121 GGAGGGCTCACGGATGGAAAGCCAAGTGAAGACCCCTGGGACAGCATGTGCTAC 1198
DEFINITION	Mus musculus	Qy 181 CCAGGGTGCATAACTCA 198
ACCESSION	U36842	Db 1181 CCAGGGTGCATAACTCA 1198
VERSION	U36842.1	RESULT 6 AF183429
KEYWORDS		
SOURCE	house mouse strain=C57 Black 6 x CBA	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 1988)	
AUTHORS	Uren, A.G., Pakusch, M., Hawkins, C.J., Puls, K.L. and Vaux, D.L.	
TITLE	Cloning and expression of apoptosis inhibitor protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors	

REFERENCE	Rattus 1 (bases 1 to 3032)	AUTHORS	Laren, R.R., Bradley, C.K., Lacher, M., Friis, R.R. and Dharmarajan, A.M.	AUTHORS	Laren, R.R., Bradley, C.K., Lacher, M., Friis, R.R. and Dharmarajan, A.M.		
AUTHORS	Dharmarajan, A.M.	TITLE	Cloning, characterization and regulation of an inhibitor of apoptosis protein in the rat corpus luteum	TITLE	Cloning, characterization and regulation of an inhibitor of apoptosis protein in the rat corpus luteum		
JOURNAL	Unpublished	JOURNAL	Unpublished	JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3032)	AUTHORS	Laren, R.R., Lacher, M., Friis, R.R. and Dharmarajan, A.M.	AUTHORS	Laren, R.R., Lacher, M., Friis, R.R. and Dharmarajan, A.M.		
AUTHORS	Direct Submission	TITLE	Submitted (08-SEP-2000) Anatomy and Human Biology, University of Western Australia, Verdun St, Nedlands, WA 6907, Australia	TITLE	Submitted (08-SEP-2000) Anatomy and Human Biology, University of Western Australia, Verdun St, Nedlands, WA 6907, Australia		
JOURNAL	Location/Qualifiers	FEATURES	source 1. .3032 /organism="Rattus norvegicus" /strain="Wistar" /product="Inhibitor of apoptosis protein 3" /protein_id="AAQAI193_1" /db_xref="GI:11890721" /clone="2" /tissue_type="ovary" /note="isolated at day 15 of pregnancy"	FEATURES	source 1. .3032 /organism="Rattus norvegicus" /strain="Wistar" /product="Inhibitor of apoptosis protein 3" /protein_id="AAQAI193_1" /db_xref="GI:11890721" /clone="2" /tissue_type="ovary" /note="isolated at day 15 of pregnancy"	FEATURES	source 1. .3032 /organism="Rattus norvegicus" /strain="Wistar" /product="Inhibitor of apoptosis protein 3" /protein_id="AAQAI193_1" /db_xref="GI:11890719" /clone="1" /tissue_type="ovary" /note="isolated at day 15 of pregnancy" 125..160 /note="TAP3" /codon_start=1 /product="Inhibitor of apoptosis protein 3" /protein_id="AAQAI193_1" /db_xref="GI:11890719" /clone="1" /tissue_type="ovary" /note="isolated at day 15 of pregnancy"
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ORIGIN		ORIGIN		ORIGIN			
Query Match	91.9% Score: 182; DB: 10; Length: 3032;	Query Match	91.1% Score: 180.4; DB: 10; Length: 2032;	Query Match	91.1% Score: 180.4; DB: 10; Length: 2032;		
Best Local Similarity	94.9%; Pred. No. 2.4e-41;	Best Local Similarity	94.4%; Pred. No. 7.2e-41;	Best Local Similarity	94.4%; Pred. No. 7.2e-41;		
Matches	188; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	Matches	187; Conservative 0; Mismatches 11; Indels 0; Gaps 0;	Matches	187; Conservative 0; Mismatches 11; Indels 0; Gaps 0;		
Db	1715 TATGAAAGCAGGATCGTTGGAACATGGATACTCAGTTAACAGGAGCCT 60	Qy	1 TATGAAGCACGGATCGTTGGAACATGGATACTCAGTTAACAGGAGCCT 60	Db	914 TATGACGCCACGGATCGTTACTTGGAACATGGCTAACAGGAGCCT 973		
Db	1774 TATGACGCCACGGATCGTTACTTGGAACATGGATACTCAGTTAACAGGAGCCT 1774	Qy	61 GGAAAGCTGGATTATTATGCTTGTAGGAGGGATAAAGTGAACTGTGGA 120	Db	974 GGAGAGCTGGATTATTATGCTTGTAGGAGGGATAAAGTGAACTGTGGA 1033		
Qy	61 GGAAAGCTGGATTATTATGCTTGTAGGAGGGATAAAGTGAACTGTGGA 120	Db	121 GGAGGCCTACGGATGGAAAGCCCTGGGACCACATGGCTAACGTGTCAC 180	Qy	121 GGAGGCCTACGGATGGAAAGCCCTGGGACCACATGGCTAACGTGTCAC 180		
Db	1775 GCAAGAGCTGGATTATTATGCTTGTAGGAGGGATAAAGTGAACTGTGGA 1834	Qy	121 GGAGGCCTACGGATGGAAAGCCCTGGGACCACATGGCTAACGTGTCAC 180	Db	1034 GGAGGCCTACGGATGGAAAGCCCTGGGACCACATGGCTAACGTGTCAC 1093		
Qy	121 GGAGGCCTACGGATGGAAAGCCCTGGGACCACATGGCTAACGTGTCAC 180	Db	1034 GGAGGCCTACGGATGGAAAGCCCTGGGACCACATGGCTAACGTGTCAC 1093	Qy	181 CCAGGGTCAAATACTCA 198		
Db	1835 GGAGGCCTACGGATGGAAAGCCCTGGGACCACATGGCTAACGTGTCAC 1894	Qy	181 CCAGGGTCAAATACTCA 198	Db	1094 CCAGGGTCAAATACTCA 1111		
Qy	181 CCAGGGTCAAATACTCA 198	Qy	181 CCAGGGTCAAATACTCA 198	Qy	181 CCAGGGTCAAATACTCA 198		
Db	1895 CCAGGGTCAAATACTCA 1912	Db	1895 CCAGGGTCAAATACTCA 1912	Db	1094 CCAGGGTCAAATACTCA 1111		
RESULT 9	E31042	RESULT 10	E31042	RESULT 10	E31042		
DEFINITION	AF304333 AF304333	LOCUS	AF304333	LOCUS	AF304333		
DEFINITION	Rattus norvegicus clone 1 inhibitor of apoptosis protein 3 mRNA, complete cds.	DEFINITION	Rattus norvegicus clone 1 inhibitor of apoptosis protein 3 mRNA, complete cds.	DEFINITION	Rattus norvegicus clone 1 inhibitor of apoptosis protein 3 mRNA, complete cds.		
ACCESSION	AF304333	ACCESSION	AF304333	ACCESSION	AF304333		
VERSION	AF304333.1	VERSION	AF304333.1	VERSION	AF304333.1		
KEYWORDS	Rattus norvegicus.	KEYWORDS	Rattus norvegicus.	KEYWORDS	Rattus norvegicus.		
ORGANISM	Rattus norvegicus. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	ORGANISM	Rattus norvegicus. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	ORGANISM	Rattus norvegicus. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
REFERENCE	1 (bases 1 to 3032)	REFERENCE	1 (bases 1 to 3032)	REFERENCE	1 (bases 1 to 1659)		

AUTHORS	Kunihiro, M.	DEFINITION	Method for screening substance inhibiting binding to XIAP.
TITLE	Method for screening substance inhibiting binding to XIAP	ACCESSION	E31042
JOURNAL	Patent: JP 1999326328-A 2 26-NOV-1999; KUNIHIRO MATSUMOTO	VERSION	E31042.1
COMMENT	OS Unidentified	KEYWORD	JP 1999326328-A/2.
ORGANISM		SOURCE	unidentified
REFERENCE	1 (bases 1 to 1659)	ORGANISM	unclassified
REFERENCE	1 (bases 1 to 1659)	REFERENCE	1 (bases 1 to 1659)

PN JP 1999326328-A/2
 PD 26-NOV-1999
 PP 13-MAY-1998 JP 1998130318
 PR
 PI KUNIHIRO MATSUMOTO
 PC G01N33/506, A61K38/00, A61K38/00, A61K38/00, A61K38/22,
 A61K39/395,
 PC A61K45/00, A61K45/00, A61K45/00, C07K7/06, C07K7/08, C07K14/47, PC
 G01N33/536,
 PC G01N33/536, G01N33/536//C12N15/09, C12P21/08, A61K37/02,
 A61K37/02, PC A61K37/02, A61K37/24, C12N15/00
 CC Strandedness: Double;
 CC Topology: Linear;
 FH Key
 FT CDS Location/Qualifiers
 82..1572.
 FEATURES SOURCE
 BASE COUNT 519 a 296 c 385 g 459 t
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 Query Match 87.4%; Score 173; DB 6; Length 1659;
 Best Local Similarity 92.4%; Pred. No. 9.4e-39;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 1 TATGAACGACGATCGTTACTTGGAACTGGATACTAGTTAACAGGAGCAGCTT 60
 Db 874 TATGAACGACGATCGTTACTTGGAACTGGATACTAGTTAACAGGAGCAGCTT 933
 QY 61 GGRAGACTGGATTATGCTTAGGTGAAGCGATAAAGTGAAAGTCCTAACATGGAA 120
 Db 934 GCAAGAGCTGGATTATGCTTAGGTGAAGCGATAAAGTGAAAGTCCTAACATGGAA 993
 QY 121 GGAGGGCTCACGGATGGAAAGCCAAGTGAAGGCCCTGGACCAGCATGCTAAGTGCTAC 180
 Db 994 GGAGGCTAACATGGATGGAAAGCCAGTGAAGGCCCTGGACCAGCATGCTAACATGGAT 1053
 QY 181 CCAGGGTGCAAATACCT 197
 Db 1054 CCAGGGTGCAAATACCT 1070
 RESULT 11
 HSU32974 HSU32974 1659 bp mRNA linear PRI 12-JUN-1996
 DEFINITION Human IAP-like protein IAP mRNA, complete cds.
 ACCESSION U32974
 VERSION U32974.1 GI:1016687
 KEYWORDS apoptosis; ring finger; zinc finger.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1659)
 REFERENCE Duckett,C.S., Nava,V.B., Gedrich,R.W., Clem,R.J., Van Dongen,J.L.,
 Gillilan,M.C., Shiels,H., Hardwick,J.M. and Thompson,C.B.
 AUTHORS
 TITLE A conserved family of cellular genes related to the baculovirus iap
 gene and encoding apoptosis inhibitors
 JOURNAL EMBO J. 15 (11), 2685-2694 (1996)
 MEDLINE 96256286
 PUBMED 8654366
 REFERENCE Duckett,C.S. and Thompson,C.B.
 AUTHORS
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-1995) Colin Duckett, Howard Hughes Medical Institute, The University of Chicago, 924 East 57th Street, Chicago, IL 60637, USA
 FEATURES SOURCE
 1. 1659 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

CDNA Library Preparation: Life Technologies, Inc.	ACCESSION	AX429575	Score 173;	DB 6;	Length 2540;	
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	VERSION	AX429575.1	GI:21540833			
DNA Sequencing by: National Institutes of Health Intramural	KEYWORDS					
Sequencing Center (NISC),	SOURCE	human.				
Gaithersburg, Maryland;	ORGANISM	Homo sapiens				
Web site: http://www.nisc.nih.gov/		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Contact: nisc_mgcnhri.nih.gov		Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Brooks, S., Blakesley, R.R., Bouffard, G.C., Breen, K., Brinkley, C., Cohen, D., Dieterich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P., Hansen, N., Ho, S.-L., Karlin, S., Kvong, P., Latic, P., Lecaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stanstrup, P.S., Thomas, P.J., Touchman, J.W., Tsui, C., Voigt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L., -H. and Green, R.D.	REFERENCE	1				
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINN at: http://image.llnl.gov	AUTHORS	Cohen, D., Dengler, U.J., Finelli, A.L., Freuler, F., Konsolaki, M., Reinhardt, M.W. and Zusman, S.				
Series: IMAK Plate: 69 Row: J Column: 18	TITLE	Transgenic drosophila melanogaster expressing beta amyloid				
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502142.	JOURNAL	PATENT: WO 0226820-A 38 04-APR-2002;				
Location/Qualifiers	FEATURES	NOVARTIS ERPTD VERWALT GMBH (AT)				
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79..1572		1. .2404				
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Matches 182; Conservative		92.4%;	Pred. No. 9.1e-39;			
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			Gaps 0;			
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Db	931	GCAAGGGCTCAGGATTGGAACTGGATAACAGGAGCTT	990			
QY	121	GGAGGGCTCAGGATTGGAACTGGATAACAGGAGCTT	180			
Db	991	GGAGGGCTCAGGATTGGAACTGGATAACAGGAGCTT	1050			
QY	181	CCAGGGTGCAGAAATCT	197			
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AX429575	ORIGIN					
LOCUS						
DEFINITION						
Query Match						
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0; Mismatches		0;	Indels 15;			
			Gaps 0;			
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QY	61	GCAAGGGCTCAGGATTGGAACTGGATAACAGGAGCTT	120			
Db	886	GCAAGGGCTCAGGATTGGAACTGGATAACAGGAGCTT	945			

Search completed: April 19, 2003, 02:09:21
Doch time : 974 secs

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using SW model

Run on: April 19, 2003, 00:03:06 ; Search time 150 Seconds
 (without alignments)
 2972.638 Million cell updates/sec

Title: US-09-654-743-51
 Perfect score: 198

Scoring table: IDENTITY-NUC
 Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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 23: /SIDS2/gcgdata/geneseq/geneseq/emb1/NA2001B.DAT;*
 24: /SIDS2/gcgdata/geneseq/geneseq/emb1/NA2002.DAT;*

Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	198	100.0	2100	18 AAT70839
2	198	100.0	2100	24 ABK93872
3	194.8	98.4	2691	19 AAV55041
4	186.3	94.3	1988	18 AAT72710
5	173	87.4	1659	21 AAT48862
6	173	87.4	2404	24 AAK9405
7	173	87.4	2540	18 AAT70836
8	173	87.4	2540	21 AAB64901
9	87.4	2540	24 ABR93869	

Key
 FH CDS
 Location/Qualifiers
 127.1617
 /*tag- a

W09706255-A2.
 XX PD 20-FEB-1997.
 XX PF 05-AUG-1996;
 XX PR 22-DEC-1995;
 XX PR 04-AUG-1995;
 XX PA 96W0-TB01022.
 XX PA 95US-0576956.
 XX PA 95US-0511485.
 PA (UYOT-) UNIV OTTAWA.

ALIGNMENTS

RESULT 1
 ID AAT70839 standard; cDNA; 2100 BP.
 AC AAT70839;

DT 02-SEP-1997 (first entry)

DE Mouse apoptosis inhibitor m-xiap cDNA.

KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; M-XIAP; HIV; AIDS; neurodegeneration; myocardial infarction; stroke; ischaemia; reperfusion injury; toxin-induced liver disease; gene therapy; diagnosis; ds.

Mus sp.

Key
 FH CDS
 Location/Qualifiers
 127.1617
 /*tag- a

XX Baird S, Korneluk RG, Liston P, Mackenzie AE;
 PI XX WPI: 1997-154262/14.
 DR XX P-PSDB; AW19584.

XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
 PT to inhibit apoptosis in, e.g., HIV or AIDS patients, and for detection
 PT of susceptible to apoptotic disease
 XX
 PS Claim 11; Page 78-79; 219pp; English.

CC Human xiap, xiap-1 and xiap-2 genes, and murine xiap, xiap-1 and
 CC xiap-2 genes (ABR7036-41) respectively code for a new class of
 CC mammalian proteins (AAW1581-86) that are inhibitors of apoptosis
 CC (IAP). The murine xiap gene (for X-linked IAP gene) sequence was
 CC constructed from 12 overlapping clones isolated from a mouse
 CC embryo lambda-gt11 cDNA library and from a mouse FIX II genomic
 CC library using human xiap cDNA as probe. IAP nucleic acids can be
 CC used to express IAP polypeptides in cells and animals to inhibit
 CC apoptosis, and as primers and probes to identify and isolate
 CC additional IAP genes, as well as in methods for treating diseases
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).
 XX Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;
 SQ Query Match 100.0%; Score 198; Length 2100;
 Best Local Similarity 100.0%; Pred. No. 1.3e-58;
 Matches 198; Conservative 0; Mismatches 0; Gaps 0;
 Db 916 PATGAGCACCAGATCCTACTTTGGAACATGGATACTCACTGAACAGGAGCTT 60
 . 916 PATGAGCACCAGATCCTACTTTGGAACATGGATACTCACTGAACAGGAGCTT 975
 . Qy 61 GCAAGAGCTGGATTATGCTTAGGTAAAGTGCACTGTGGA 120
 . 976 GCAAGAGCTGGATTATGCTTAGGTAAAGTGCACTGTGCTACTGTGGA 1035
 Db 121 GGAGGGCTCACGGATTGGAAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAC 180
 . 1036 GGAGGGCTCACGGATTGGAAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAC 1095
 Qy 181 CCAGGGTGCATAATACCTA 198
 Db 1096 CCAGGGTGCATAATACCTA 1113

RESULT 2
 ABK93872 ID ABK93872 standard; cDNA; 2100 BP.
 XX AC ABK93872;
 DT 26-AUG-2002 (first entry)
 XX DE Mouse cDNA encoding inhibitor of apoptosis, XIAP.

XX Mouse; ss: gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.

XX OS Mus sp.
 XX PN WO200226968-A2.
 PD 04-APR-2002.
 XX PP 27-SEP-2001; 2001WO-CA01379.
 XX PR 28-SEP-2000; 2000US-0672717.

XX RESULT 3
 AAV55041 ID AAV55041 standard; cDNA; 2691 BP.
 DE Murine XIAP coding sequence.
 XX AC AAV55041;
 XX AC AAV55041;
 XX DT 13-NOV-1998 (first entry)
 XX DE Murine XIAP coding sequence.
 XX KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein; ss.
 XX OS Mus sp.
 XX PR Key Location/Qualifiers

FT 672..2162
/*tag= a
/product= XIAP
XX WO9835693-A2.
XX 20-AUG-1998.
XX PF 13-FEB-1998; 98RO-IB00781.
XX PR 13-FEB-1997; 97US-0800929.
XX PA (UYOT-) UNIV OTTAWA.
XX PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
PI Tsang B;
XX DR WPI,1998-467164/40.
XX PT P-PDB; AAW69297.
XX PT Inducing apoptosis in proliferative mammalian cells with inhibitor
PT of IAP or NAIP polypeptide - also methods for prognosis based on
PT presence of IAP and NAIP, specifically applied to cancers involving
PT p53 mutations
XX PS Claim 13: Fig 4; 147pp; English.
XX CC This sequence encodes the mouse XIAP protein, which is an inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis.
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors
XX Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 other.
SQ Query Match 98.4%; Score 194.8; DB 19; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1.9e-57;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 1 1ATGAGACGGATGGATTATGGAAACATGGATAATCGTTAACAGGASCAGCTT 60
Db 1461 TATGAGGCAGGATTATGGTTACTTGGAAATGGCTCCACTGTGGA 1520
Qy 61 GCAAGAGCAGGATTATGGAAATGGCTCCACTGTGGA 120
Db 1521 GCAAGAGCAGGATTATGGAAATGGCTCCACTGTGGA 1580
Qy 121 GGAGGGCTACGGATTGGAGGCCAAGTGAGACCCCTGGGACCCATGTAAGTGCTAC 180
Db 1581 GGAGGGCTACGGATTGGAGGCCAAGTGAGACCCCTGGGACCCATGTAAGTGCTAC 1640
Qy 181 CCAGGGTGCRAATACTCA 198
Db 1641 CCAGGGTGCRAATACTCA 1658

RESULT 4
AAT7210 ID AAT7710 standard; DNA; 1988 BP.
XX AC AAT7210;
XX DT 16-SEP-1997 (first entry)

RESULT 5
AAZ48862 ID AAZ48862 standard; cDNA; 1659 BP.
XX

AC	AAZ48862;		AC	AAK9405;	
XX		XX	XX	XX	
DT	24-MAR-2000	(first entry)	DT	27-JUN-2002	(first entry)
XX	Human XIAP coding sequence.		XX	DE	DNA of APP related human homologue hCP35211.
DE			XX	DE	DNA of APP related human homologue hCP35211.
XX			XX	KW	Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta; amyloid precursor protein; tissue-specific expression control; human APP; APP Pathway modulator; gene therapy; gene; ds.
KW	Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta; transforming growth factor-beta activated kinase 1; monocyte migration; TAK1 binding protein 1; extracellular matrix protein production; cell growth inhibitor; beta-amyloid protein deposition; immunosuppression; transforming growth factor-beta; ds.		XX	KW	APP Pathway modulator; gene therapy; gene; ds.
KW			XX	KW	OS Homo sapiens.
XX			XX	OS	
OS			XX	XX	
XX			XX	XX	
PN	JP11326328-A.		Key	Key	Location/Qualifiers
XX			CDS	CDS	692..1528
PD	26-NOV-1999.		FT	FT	/tag= a
XX			PF	FT	/product= "Protein of human homologue hCP35211"
DR	WPI; 2000-078337/07.		XX	FT	/note= "No start codon"
XX			XX	XX	
PS	13-MAY-1998;	98JJP-0130378.	PN	W0200226820-A2.	
XX			XX	XX	
PR	13-MAY-1998;	98JJP-0130378.	PD	04-APR-2002	
XX			XX	XX	
PA	(MATS/)	MATSUMOTO K.	PP	01-OCT-2001;	2001WO-EP11345.
XX			XX	XX	
PA	WPI; 2000-078337/07.		PR	29-SEP-2000;	2000US-236899P.
DR	P-PSDB; AAY59451.		PR	14-JUN-2001;	2001US-298309P.
XX			XX	XX	
PT	Screening a substance which inhibits combination of the X-linked		PA	(NOV/) NOVARTIS AG.	
PT	inhibitor of apoptosis protein -		PA	(NOV/) NOVARTIS-ERFINDUNGEN VERW GES MBH.	
XX			XX	XX	
PS	Disclosure; Page 28-30; 43pp; Japanese.		PI	Cohen D, Dengler UJ, Pinelli AL, Freuler F, Konsolaki M;	
XX			PI	Reinhardt NWHM, Zusman S;	
CC	This sequence encodes the human XIAP protein.		XX	XX	
CC	The invention relates to a method for screening a substance inhibiting		DR	WPI; 2002-315796/35.	
CC	the formation of a complex between XIAP and TAB1, in which X-linked		DR	P-PSDB; AAO20511.	
CC	inhibitor of apoptosis protein (XIAP), transforming growth factor-beta		XX	XX	
CC	activated kinase 1 (TAK1) binding protein 1(TAB1) and a substance to be		PT	New transgenic fly, containing DNA encoding an Abeta portion of human	
CC	tested are contacted with each other and then the presence or formation		PT	APP, useful for identifying agents which modulate the APP pathway and	
CC	of a complex between XIAP and TAB1 is detected. The substance can be used		PT	which can be used to treat Alzheimer's disease -	
CC	as a drug for extracellular matrix protein production enhancement, cell		XX	Example 4; Page 111; 129PP; English.	
CC	growth inhibition, monocyte migration, physiologically active substance		XX	CC The invention relates to a polypeptide having the Abeta portion of human amyloid	
CC	induction, immunosuppression, and beta-amyloid protein deposition. A		CC	precursor protein (APP), fused to a signal sequence. The DNA sequence	
CC	substance inhibiting the formation of a complex between TAB1 and XIAP as		CC	encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in	
CC	well as between XIAP and TGF-beta (transforming growth factor-beta) type		CC	the specific expression control sequence. Expression of the sequence gives	
CC	I and/or type II receptor is useful as a drug.		CC	the fly an altered phenotype. The purpose of the invention is for	
XX			CC	identifying agents that inhibit or promote the expression and/or function	
SQ	Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;		CC	of genes or encoded polypeptides which modify the APP pathway. The agent	
Query Match	Score 173; DB 21; Length 1659;		CC	is a compound, triple helix DNA, antisense oligonucleotide, double	
Best Local Similarity	97.4%; Pred. No. 6..3e-50;		CC	stranded RNA molecule, ribozyme, or particularly an antibody. It is used	
Matches 182; Conservative	0; Mismatches 15; Indels 0; Gaps 0;		CC	to treat conditions such as Alzheimer's disease. The agent can be used as	
Qy	1 TATGAACTGAGCATGTTACTTGTGAACTGGATACTCGAGTAAAGGAGCAGCTT		CC	an APP pathway modulator or in gene therapy. This polynucleotide sequence	
Db	874 TATGAACTGAGCATGTTACTTGTGAACTGGATACTCGAGTAAAGGAGCAGCTT		CC	represents the DNA of the APP related human homologue hCP35211.	
Qy	61 GGAAGACTGATTTATGCTTAGGTAAAGGCATAAACTGAAGTCAGTCACTGTGGA		XX	Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 other;	
Db	934 GGAAGACTGATTTATGCTTAGGTAAAGGCATAAACTGAAGTCAGTCACTGTGGA		Qy	Match 87.4%; Score 173; DB 24; Length 2404;	
Qy	933 GGAAGACTGATTTATGCTTAGGTAAAGGCATAAACTGAAGTCAGTCACTGTGGA		Db	Best Local Similarity 92.4%; Pred. No. 7.3e-50;	
Db	180 GGAAGACTGATTTATGCTTAGGTAAAGGCATAAACTGAAGTCAGTCACTGTGGA		Db	Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;	
Qy	181 CGAGGTCAGGATCAATCT 197		Qy	1 TATGAACTGAGCATGTTACTTGTGAACTGGATACTCGAGTAAAGGAGCAGCTT	
Db	1054 CGAGGTCAGGATCAATCT 1070		Db	887 GCAAGACCTGAGCTTACGTTACGTTACGTTACGTTACGTTACGTTACGTT	
RESULT 6			Qy	61 GCAAGAGCTGGATTATGCTTAGGTAAAGGCATAAACTGAAGTCAGTCACTGTGGA	120
AAK99405			Db	886 GCAAGACCTGAGCTTACGTTACGTTACGTTACGTTACGTTACGTTACGTT	886
ID AAK99405 standard; DNA: 2404 BP.			Qy	121 GGAGGGCTCAGGATGGAACTGAAAGCCCTGGGACCCAGTGAACTGCTAACATGTA	946
XX			Db	122 GGAGGGCTCAGGATGGAACTGAAAGCCCTGGGACCCAGTGAACTGCTAACATGTA	180

Db 947 GGAGGCTAACTGATTGAAAGCCGAGTGAAGACCCCTGGAAACAATGCTAAATGGAT 1006
 QY 181 CCAGGGTGCAATACCT 197
 Db 1007 CCAGGGTGCAATATCT 1023

RESULT 7
 AAT70836 ID AAT70836 standard; cDNA; 2540 BP.
 XX AC AAT70836;
 XX DT 02-SEP-1997 (first entry)
 DE Human apoptosis inhibitor xiap cDNA.
 XX KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;
 KW XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;
 KW ischaemia; myocardial infarction; stroke;
 KW reperfusion injury; toxin-induced liver disease; gene therapy;
 KW diagnosis; ds.
 OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT CDS 34..1527 /*tag= a
 XX PN WO9706255-A2.
 XX PD 20-FEB-1997.
 XX PF 05-AUG-1996; 96WO-TB01022.
 XX PR 22-DEC-1995; 95US-0576056.
 PR 04-AUG-1995; 95US-051485.
 PA (UYOT-) UNIV OTTAWA.
 PI Baird S, Kornbluk RG, Liston P, Mackenzie AE;
 XX WPI: 1997-154262/14.
 DR P-PSDB; AW19581.
 XX PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
 PT of susceptibility to apoptotic disease
 XX PS Claim 12: Page 67-68; 219pp; English.
 XX CC Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and
 CC hiap-2 genes (AAU036-41) respectively code for a new class of
 mammalian proteins (AAU19581-86) that are inhibitors of apoptosis
 (IAP). The xiap gene (for X-linked IAP gene) was isolated from a
 CC human foetal brain ZapiII cDNA library using an X-linked sequence
 CC tag site that shows strong homology with the conserved ring Zinc
 CC finger domain of baculovirus CpiAP and OpiAP genes. The gene was
 CC assigned to chromosome Xq25 by FISH. IAP nucleic acids can be used
 CC to express IAP polypeptides in cells and animals to inhibit
 CC apoptosis, and as primers and probes to identify and isolate
 CC additional IAP genes, as well as in methods for treating diseases
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).
 XX SQ Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 1 other;
 Query Match 87.4%; Score 173; DB 18; Length 2540;
 Best Local Similarity 92.4%; Pred. No. 7.5e-50;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 948 GGAGGCTCAAGGTGGAAACCTGGATAACTCAGTAACAGGACAGCTT 60
 XX AC AAT70836 standard; cDNA; 2540 BP.
 XX DT 07-NOV-2000 (first entry)
 DE Human X-linked inhibitor of apoptosis DNA.
 XX KW X-linked inhibitor of apoptosis; XIAP; hIAP; MIHA; U45880;
 KW antisense; antiinflammatory; cytostatic; tumour; ds.
 OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT CDS 34..1527 /*tag= a
 /product= "X-linked inhibitor of apoptosis"
 XX PN US6087173-A.
 XX PD 11-JUL-2000.
 XX PF 09-SEP-1999; 99US-0392580.
 XX PR 09-SEP-1999; 99US-0392580.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Bennett CF, Cowser LM, Ackermann EJ;
 XX DR WPI: 2000-498201/44.
 DR P-PSDB; AW19585.
 XX PT Antisense compound useful for research reagents, diagnostics,
 PT prophylaxis and for treating disorders associated with X-linked
 inhibitor of apoptosis, modulates expression of X-linked inhibitor of
 PT apoptosis.
 XX Example 13: Column 43-48; 33pp; English.
 XX CC The present invention relates to antisense oligonucleotides designed to
 CC inhibit expression of the human X-linked inhibitor of apoptosis. The
 CC present sequence is the X-linked inhibitor of apoptosis DNA.
 CC Modified phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are
 CC more effective inhibitors than unmodified oligonucleotides. The
 CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
 CC expression in cells and tissues in vitro. The oligonucleotides are also
 CC useful for treating animals or humans, prone to a disease associated
 CC with X-linked inhibitor of apoptosis. The oligonucleotides may also be
 CC used prophylactically to prevent infection, inflammation or tumour
 CC formation.
 XX SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 other;
 Query Match 87.4%; Score 173; DB 21; Length 2540;
 Best Local Similarity 92.4%; Pred. No. 7.5e-50;
 Matches 182; Conservative 0; Mismatches 15; Indels 1; Gaps 0;

QY	1	TATGAAAGCACGGACCTTCACTTTGGAAACATCTCAGTAGATAACAGGGCAGCTT	60
DDB	826	TATGAAAGCACGGACCTTCACTTTGGAAACATCTCAGTAGATAACAGGGCAGCTT	120
QY	61	GCAAGAGCTGGATTATGCTTTAAGTGAAACTGATAAGTGAAGTCGTCCACTGTGGA	120
DDB	886	GCAAGAGCTGGATTATGCTTTAAGTGAAACTGATAAGTGCCTTACTGTGGA	945
QY	121	GGAGGGCTCACGGATGGCAGTGGCAGTGAACTGAGACCCCTGGGACCACATGCTAAGTCGTAC	180
DDB	946	GGAGGGCTAACATGGTAACCTGGAAACCCCATGGACCCCTGGACACATGCTAAATGTT	1005
QY	181	CCAGGGTGCAAATACTCT	197
DDB	1006	CCAGGGTGCAAATACTCT	1022
RESULT 9			
	ABK93869	standard; cDNA; 2540 bp.	
XX	ABK93869;		
XX		26-AUG-2002 (first entry)	
XX		Human cDNA encoding inhibitor of apoptosis, XIAP #1.	
XX		HUMAN ss; gene; antisense; inhibitor of apoptosis; XIAP1; XIAP2; XIAP; cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer; embryonic development; viral pathogenesis; autoimmune disorder; neurodegenerative disease; multiple sclerosis; lupus erythematosus; herpes virus infection; pox virus infection; adenovirus infection; proliferative disease.	
XX		Homo sapiens.	
OS		WO200226968-A2.	
XX		04-APR-2002.	
XX		27-SEP-2001; 2001WO-QA01379.	
XX		28-SEP-2000; 2000US-0672717.	
PA		(UYOT-) UNIV OTTAWA.	
PA		(AEGE-) AEGERA THERAPEUTICS INC.	
XX		Korneluk RG, Lacasse E, Baird S, Holch M, Young S;	
PI		WPI: 2002-479562/51.	
XX		P-PSDB: ABG65663.	
XX		Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing apoptosis in a cell, for treating cancer and other proliferative diseases	
XX		Disclosure: Fig 1; 135pp; English.	
XX		The invention relates to an inhibitor of apoptosis (IAP) antisense nucleic acid (1) that inhibits IAP biological activity, regardless of length of the antisense nucleic acid, the IAP proteins may be mouse or human XIAP, XIAP1 or XIAP2. Also included are a pharmaceutical composition comprising a mammalian IAP antisense molecule and a method enhancing apoptosis in a cell, comprising administering a negative regulator of the IAP anti-apoptotic pathway to the cell. The IAP antisense inhibitor is useful for enhancing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for treating a patient diagnosed with a proliferative disease like cancer. The IAP antisense molecule is useful to treat, ameliorate, improve, sustain or prevent proliferative diseases (e.g. ovarian cancer, colon cancer, lymphoma, pancreatic cancer), and also in embryonic conditions where apoptosis is involved or implicated (e.g. embryonic denocarcinoma, lymphoma).	

enhancing apoptosis in a cell, comprising administering a negative regulator of the IAP anti-apoptotic pathway to the cell. The IAP antisense inhibitor is useful for enhancing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for treating a patient diagnosed with a proliferative disease like cancer. The IAP antisense molecule is useful to treat, ameliorate, improve, sustain or prevent proliferative diseases (e.g. ovarian cancer, adenocarcinoma, lymphoma, pancreatic cancer) and also in diseases or conditions where apoptosis is involved or implicated (e.g. embryonic development, viral pathogenesis, autoimmune disorders, neurodegenerative diseases, multiple sclerosis, lupus erythematosus and infection by herpes viruses, pox virus and adenovirus). The present sequence is a human IAP cDNA sequence.

XX 05-APR-2001.
 XX 29-SEP-2000; 2000WO-US26735.
 XX PR 30-SEP-1999; 99US-0157169.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PPI Duckett C, Mir SS;
 XX DR P-PSDB; AHE00359.
 XX P1 Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with transforming growth factor beta receptor modulating activity, and the nucleic acids that encode them, useful for treating, e.g. diabetes and multiple sclerosis .
 XX PS Claim 18; Page 87-88; 108pp; English.
 CC The present sequence is human inhibitor of apoptosis (IAP)-like protein-3 (ILP-3) cDNA. The hILP-3 gene is located on chromosome 2q12-q14.
 CC ILP-3 comprises a spacer region and a ring finger domain. The ILP-3 interacts with transforming growth factor beta receptor (TGFbetaR) and mediates TGFbetaR activity. ILP-3 also moderately inhibits ILP-1 mediated c-Jun N-terminal kinase (JNK) activation when co-transfected with ILP-1. Such activity decreases or prevents apoptosis in cell.
 CC ILP-3 is used in the area of genetic testing for predisposition to diseases, such as osteoarthritis, hypothyroidism, juvenile nephrophthisis, thrombophilia, colorectal cancer and neonatal purpura fulminans owing to an ILP-3 deletion or mutation. The ILP is also used in the treatment of diseases associated with abnormal apoptosis such as cancer, autoimmune diseases, e.g., diabetes and multiple sclerosis and neurodegenerative diseases including retinal degeneration. The ILP-3 gene is also used in gene therapy for treating patients suffering from ILP-3 gene deletions or mutations.
 SQ Sequence 1752 BP; 530 A; 299 C; 385 G; 538 T; 0 other;
 Query Match 79.3%; Score 157; DB 22; Length 1752;
 Best Local Similarity 87.3%; Pred. No. 2.4e-44;
 Matches 172; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
 QY 1 TATGAGCACCAGATCCCTACTTTGGAAACATGGATACTCGTTAACARGAGGAGCTT 60
 DB 499 TATGAGCATGATCATTTACTTTGGATGTGGATATTCACTAAGGAGGAGCTT 558
 QY 61 GCAAGAGCTGGATTATATGCTTACTGTGAACTGATAAGTGAAGTGCTTCACGTGTTGA 120
 DB 559 TCAAGAGCTGGATTATATGCTTACTGTGAACTGATAAACTGTTAACATGGCTTACGTGTTGA 618
 QY 121 CGAGGGCTCAGGGATGAACTGAAACCCCTGGACCACTGTAAGTGCTAC 180
 DB 619 GGGGGCTAACTGATGGAAACGCCAGCGAAGACCCCTTGGSAACAACTGATAAATGGCAT 678
 QY 181 OCAGGGTCAAATACCT 197
 DB 679 CCAGGGTCAAATACCT 695

RESULT 13
 ABK14677 ID ABK14677 standard; CDNA; 1758 BP.
 XX AC ABK14677;
 XX DB 08-MAY-2002 (first entry)
 XX DE Human Inhibitor of apoptosis protein 7 (IAPL7) cDNA.
 KW Human; gene; inhibitor of apoptosis protein 7; IAPL7; cytostatic;
 KW antiapoptotic; IAP; apoptosis; antibody; V-Rel; NF-kappaB;

KW chromosome 19; vaccine; gene therapy; hyperproliferative disease;
 KW cancer; transgenic animal; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT CDS 286..1680
 FT /*tag= a */product= "IAPL7 protein"
 FT FT /partial_ "/note= "No start codon shown"
 XX PN WO200210381-A1.
 XX PD 07-FEB-2002.
 XX P1 18-JUL-2001; 2001WO-EP08287.
 XX PR 28-JUL-2000; 2000EP-0116452.
 XX PA (MERE) MERCK PATENT GMBH.
 XX P1 Hentsch B;
 XX DR 2002-188741/24.
 XX PR AAU75747.
 XX PA New inhibitor of apoptosis proteins and polynucleotides useful in PT New inhibitor of apoptosis proteins and polynucleotides useful in PT vaccines for inducing an immune response against hyperproliferative PT diseases e.g. cancer -
 XX PS Claim 5; Page 33-35; 41pp; English.
 CC This invention relates to the nucleic acid and protein sequences of a novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences have homology to the IAP (Inhibitors of apoptosis) gene family which are thought to inhibit proteins by regulating the anti-apoptotic activity of the V-Rel and NF-kappa B family of transcription factors.
 CC The gene for IAPL7 is located on human chromosome 19. The nucleic acids of the invention are useful for screening to identify compounds that stimulate or inhibit the function or level of IAPL7, where the identified compounds are useful for treating hyper proliferative diseases such as cancer. The protein sequences may also be used to identify membrane bound or soluble receptors of IAPL7 by standard receptor binding techniques. Nucleic acids encoding IAPL7, may be used as hybridisation probes for cDNA and genomic DNA, or as primers for nucleic acid amplification reaction and the primers and probes may also be used to isolate full-length cDNAs and genomic clones encoding IAPL7.
 CC The nucleic acid sequences are useful as diagnostic reagents for diagnosing a disease or a susceptibility to a disease by detecting mutations in the associated gene. The nucleic acid sequence is useful for chromosome localisation and tissue expression studies and is also useful for producing transgenic animals. The IAPL7 protein sequence may also be used to generate an anti-IAPL7 antibody which is useful in screening methods for detecting the effect of added compounds on the production of mRNA and protein in cells. The sequences of the invention are also useful as vaccines for inducing an immunological response in a mammal. The present sequence represents the cDNA encoding the human inhibitor of apoptosis 7 (IAP7) protein of the invention.
 XX SQ Sequence 1758 BP; 488 A; 371 C; 470 G; 429 T; 0 other;
 Query Match 75.3%; Score 149; DB 24; Length 1758;
 Best Local Similarity 84.8%; Pred. No. 1.5e-41;
 Matches 167; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 QY 1 TATGAGCACCAGATCCCTACTTTGGAAACATGGATACTCGTTAACARGAGGAGCTT 60
 DB 979 TATGAGCATGATCATTTACTTTGGATGTGGATATTCACTAAGGAGGAGCTT 1038
 QY 61 GCAAGAGCTGGATTATATGCTTACTGTGAACTGATAAGTGAAGTGCTTCACGTGTTGA 120
 DB 1039 GCAGAGCTGGATTATGCTTACGTGAACTGATAAACTGATAAATGGCAT 1098

QY 121 GGAGGGCAGCGATTGGAAAGCCAAAGTGAAGACCCCTGGGACCACATGCTAC 180
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1099 GGAGGGCTGCCAACTGGGAGCCAAAGGAGATCCTGGAAACCCATSCATAATGGTAT 1158
 QY 181 CCAAGGGAAATACCT 197
 Db 1159 CCAAGGGAAATACCT 1175

RESULT 14

ID ABK14678 standard; cDNA: 1758 BP.
 XX ID ABK14678;
 AC AC
 DT 08-MAY-2002 (first entry)
 XX Human Inhibitor of apoptosis protein 7 (IAPL7) cDNA #2.
 DE Human; gene; inhibitor of apoptosis 7; IAPL7; cycostatic; antilapoptotic; IAP; apoptosis; V-Rel; NF-kappaB; antibody; chromosome 19; vaccine; gene therapy; hyperproliferative disease; cancer; transgenic animal; ss.
 KW Homo sapiens.
 XX Location/Qualifiers
 FH Key 286..687
 FT FT /*tag= a
 FT FT /product= "IAPL7 protein"
 FT FT /note= "This sequence encodes amino acid residues 1-133 of the protein shown in AAU5747. No start codon shown."
 FT FT
 XX WO200210381-A1.
 PN PD 07-FEB-2002.
 XX PP 18-JUL-2001; 2001WO-EP003287.
 XX PR 28-JUL-2000; 2000EP-0116452.
 XX PA (MERE) MERCK PATENT GMBH.
 PI Hentsch B;
 XX DR WPI; 2002-188741/24.
 PT New inhibitor of apoptosis proteins and polynucleotides useful in vaccines for inducing an immune response against hyperproliferative diseases e.g. cancer -
 XX PS Claim 5; Page 36-38; 41pp; English.

This invention relates to the nucleic acid and protein sequences of a novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences have homology to the IAP (inhibitors of apoptosis) gene family which are thought to inhibit proteins by regulating the anti-apoptotic activity of the V-Rel and NF-kappaB family of transcription factors. The gene for IAPL7 is located on human chromosome 19. The nucleic acids of the invention are useful for screening to identify compounds that stimulate or inhibit the function or level of IAPL7, where the identified compounds are useful for treating hyper proliferative diseases such as cancer. The protein sequences may also be used to identify membrane bound or soluble receptors of IAPL7 by standard receptor binding techniques. Nucleic acids encoding IAPL7, may be used as hybridisation probes for cDNA and genomic DNA, or as primers for nucleic acid amplification reaction and the primers and probes may also be used to isolate full-length cDNAs and genomic clones encoding IAPL7. The nucleic acid sequences are useful as diagnostic reagents for diagnosing a disease or a susceptibility to a disease by detecting

mutations in the associated gene. The nucleic acid sequence is useful for chromosome localisation and tissue expression studies and is also useful for producing transgenic animals. The IAPL7 protein sequence may also be used to generate an anti-IAPL7 antibody which is useful in screening methods for detecting the effect of added compounds on the production of mRNA and protein in cells. The sequences of the invention are also useful as vaccines for inducing an immunological response in a mammal. The present sequence represents the human inhibitor of apoptosis 7 (IAP7) cDNA #2 of the invention. This sequence is the same as the sequence shown in ABK14677 but has a stop codon at nucleotide 685-687.

XX Sequence 1758 BP; 489 A; 371 C; 470 G; 428 T; 0 other;
 SQ Query Match 75.3%; Score 149; DB 24; Length 1758;
 ID Best Local Similarity 84.8%; Pred. No. 1.5e-41;
 AC Matches 167; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 DT Matches 167; Conservatve 0; Mismatches 30; Indels 0; Gaps 0;
 XX QY 1 TATGGAAAACGGATCCATTACTTTGGAAACATGGATTAATCTAGTAAAGGAGAGCTT 60
 Db 979 TATGAGGCCGGCTCATTTACTTTGGACATGGATTAATCGGTAAAGGAGCTT 1038
 QY 61 GCAAGAGCTGGATTATTCATGCTTATGGTAAAGTGAAGTGAAAGTGCATCTGCACTGTGGA 120
 Db 1039 GCAAGAGCTGGATTATTCATGCTTATGGTAAAGTGAAGTGAAAGTGCATCTGCACTGTGGA 1098
 QY 121 GGAGGGCTCAGGGATGGAAAGCCAAAGTGGACCAGCATGCTAACGCTAC 180
 Db 1099 GGAGGGCTAGGCCAACTGGAAAGCCCAGGAACATGGTAAAGCATGGTAT 1158

RESULT 15

ID AAD03381 standard; cDNA; 4993 BP.
 XX ID AAD03381 standard; cDNA; 4993 BP.
 AC AC
 XX AAD03381;
 DT 19-JUN-2001 (first entry)
 XX DE Human IAP-like protein-2 (ILP-2) cDNA.
 XX DE Human, inhibitor of apoptosis; IAP-like protein-2; ILP-2;
 KW chromosome 19q13.3-q13.4; transforming growth factor beta receptor;
 KW TGFbeta2R; c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;
 KW cone-rod retinal dystrophy 2; retinitis pigmentosa; colorectal cancer;
 KW T-cell acute lymphoblastic leukaemia; neurodegenerative disease;
 KW retinal degeneration; hyperferritinæmia-cataract syndrome; cancer;
 KW autoimmune disease; diabetes; multiple sclerosis; cytostatic; ss.
 OS Homo sapiens.
 XX Key
 FN CDS 2074..2784
 FT /*tag= a
 FT /product= "Human inhibitor of apoptosis (IAP)-like protein-2 (hILP-2)"
 FT protein-2 (hILP-2)"
 XX WO200123568-A2.
 XX DE 05-APR-2001.
 XX FT 29-SEP-2000; 2000WO-US26735.
 XX FT 30-SEP-1999; 99US-0157169.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Duckett C, Mir SS;
 XX DR WPI; 2001-258135/26.

DR P-PSDB: AAE00365.
 XX
 PT Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
 PT transforming growth factor beta receptor modulating activity, and the
 PT nucleic acids that encode them, useful for treating, e.g. diabetes and
 PT multiple sclerosis -
 XX

PS Claim 18; Page 94-98; 108pp; English.

XX
 CC The present sequence is human inhibitor of apoptosis (IAP)-like protein-2
 CC (ILP-2) cDNA. The ILP-2 gene is located on chromosome 19q13.3-q13.4.
 CC ILP-2 comprises a single amino-terminal domain known as baculovirus iap
 CC repeat (BIR), followed by a spacer region and a carboxy-terminal ring
 CC finger domain. It interacts with transforming growth factor beta
 CC receptor (TGFbetaR) and modulates TGFbetaR activity. It also potently
 CC inhibits apoptosis induced by overexpression of Bax or by Caspase-9 and
 CC Apaf-1. It also activates c-Jun N-terminal kinase (JNK) activity. ILP-2
 CC is used in the area of genetic testing for predisposition to diseases,
 CC such as cone-rod retinal dystrophy-2, retinitis pigmentosa,
 CC glaucomatiduria, T-cell acute lymphoblastic leukaemia, colorectal cancer
 CC and hyperferritinæmia-cataract syndrome owing to an ILP-2 deletion or
 CC mutation. The ILP is also used in the treatment of diseases associated
 CC with abnormal apoptosis such as cancer, autoimmune diseases, e.g.,
 CC diabetes and multiple sclerosis and neurodegenerative diseases including
 CC retinal degeneration. The ILP-2 gene is also used in gene therapy for
 CC treating patients suffering from ILP-2 gene deletions or mutations.
 XX

SQ Sequence 4993 BP; 1526 A; 973 C; 1196 G; 1297 T; 1 other;

Query Match 75.3%; Score 149; DB 22; Length 4993;
 Best Local Similarity 84.8%; Pred. No. 2.3e-41;
 Matches 167; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy	1	TATGAAACAGGATCGTTACTGGTAACTGGATAACAGGAGGAGCTT
Db	2083	TATGAAACCCGGCTCATTTACTTTGGACATGGTAGTCGTTAACAGGAGCTT
Qy	61	GCAGAGCTGGATTTATGCTTATGGTAGGTGAAGGGATAAAGTGAGTGCTTCAGTGGA
Db	2143	
Qy	121	GGAGGGCTCAGGATGGAAAGCCAAGTGAAGACCCCTGGACAGCATGCTAAGTGCTA
Db	2203	
Qy	181	CCAGGGTAGCCAACGGACGCCAAGGAATCTTGGAACAGCATCTAAATGGTAT
Db	2263	

Search completed: April 19, 2003, 01:52:57
 Job time : 157 secs

RESULT 3
 US-08-800-929A-9
 Sequence 9, Application US/08800929A
 Patent No. 6133437
 GENERAL INFORMATION:
 ; APPLICANT: Korneiuk, Robert G

Db 916 TATGAAACGGATCGTTACTTTGGAACATGGATACTACAGTAAACAGGACAGCTT 975
 Qy 61 GCAAGAGCTGGATTATGGTTAGGTGAGGGCATANOTGAGTGCTCCACTGTGGA 120
 Db 976 GCAAGAGCTGGATTATGGTTAGGTGAGGGCATAAAGTGAGTGCTCCACTGTGGA 1035
 Qy 121 GGAGGCCTCACGGATTGGAAAGCCAAAGTGAAGCCAGATGTAATGTCTAC 180
 Db 1036 GGAGGCCTCACGGATTGGAAAGCCAAAGTGAAGCCAGATGTAATGTCTAC 1095
 Qy 181 CCAGGGTGCATAATACCTA 198
 Db 1096 CCAGGGTGCATAATACCTA 1113

RESULT 2
 US-09-212-971-9
 Sequence 9, Application US/09212971B
 GENERAL INFORMATION:
 ; APPLICANT: Korneiuk, Robert G
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Tsang, Stephen
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; FILE REFERENCE: 07851/009002
 ; CURRENT APPLICATION NUMBER: US/09/212-971B
 ; CURRENT FILING DATE: 1998-12-16
 ; EARLIER APPLICATION NUMBER: 60/017, 354
 ; EARLIER FILING DATE: 1996-04-26
 ; EARLIER APPLICATION NUMBER: 60/030, 590
 ; EARLIER FILING DATE: 1996-11-14
 ; EARLIER APPLICATION NUMBER: 08/800, 9229
 ; EARLIER FILING DATE: 1997-02-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FASSEQ for Windows Version 4.0
 ; SEQ ID NO: 9
 ; LENGTH: 2691
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; US-09-212-971-9

Query Match 98.4%; Score 194; DB 3; Length 2691;
 Best Local Similarity 99.0%; Pred. No. 1.9e-60;
 Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TATGAAACGGATCGTTACTTTGGAACATGGATACTACAGTAAACAGGACAGCTT 60
 Db 1461 TATGAAACGGATCGTTACTTTGGAACATGGATACTACAGTAAACAGGACAGCTT 1520
 Qy 61 GCAAGAGCTGGATTATGGTTAGGTGAGGGCATAAAGTGAGTGCTCCACTGTGGA 120
 Db 1521 GCAAGAGCTGGATTATGGTTAGGTGAGGGCATAAAGTGAGTGCTCCACTGTGGA 1580
 Qy 121 GGAGGCCTCACGGATTGGAAAGCCAAAGTGAAGCCAGATGCTAATGTCTAC 180
 Db 1581 GGAGGCCTCACGGATTGGAAAGCCAAAGTGAAGCCAGATGCTAATGTCTAC 1640
 Qy 181 CCAGGGTGCATAATACCTA 198
 Db 1641 CCAGGGTGCATAATACCTA 1658

Query Match 98.4%; Score 194; DB 3; Length 2691;
 Best Local Similarity 99.0%; Pred. No. 1.9e-60;
 Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TATGAAACGGATCGTTACTTTGGAACATGGATACTACAGTAAACAGGACAGCTT 60
 Db 1461 TATGAAACGGATCGTTACTTTGGAACATGGATACTACAGTAAACAGGACAGCTT 1520
 Qy 61 GCAAGAGCTGGATTATGGTTAGGTGAGGGCATAAAGTGAGTGCTCCACTGTGGA 120
 Db 1521 GCAAGAGCTGGATTATGGTTAGGTGAGGGCATAAAGTGAGTGCTCCACTGTGGA 1580
 Qy 121 GGAGGCCTCACGGATTGGAAAGCCAAAGTGAAGCCAGATGCTAATGTCTAC 180
 Db 1581 GGAGGCCTCACGGATTGGAAAGCCAAAGTGAAGCCAGATGCTAATGTCTAC 1640
 Qy 181 CCAGGGTGCATAATACCTA 198
 Db 1641 CCAGGGTGCATAATACCTA 1658

RESULT 4
 US-09-617-053A-9
 Sequence 9, Application US/09617053A
 ; Sequence 9, Application US/09617053A
 ; Patient No. 6130492
 ; GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G
 APPLICANT: Mackenzie, Alexander E
 APPLICANT: Lister, Peter
 APPLICANT: Baird, Stephen
 APPLICANT: Tsang, Benjamin K
 APPLICANT: Pratt, Christine
 TITLE OF INVENTION: NAIF FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
 TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 TITLE OF INVENTION: DISSEASE
 FILE REFERENCE: 07891/003003
 CURRENT APPLICATION NUMBER: US/09/617,053A
 CURRENT FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US 08/800,929
 PRIOR FILING DATE: 1997-02-13
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 9
 LENGTH: 2691
 TYPE: DNA
 ORGANISM: Mus musculus
 US-09-617-053-A-9

RESULT 6
 US-08-511-185-3
 Sequence 3 Application US/08511485
 Patent No. 591912
 GENERAL INFORMATION:
 APPLICANT: Korneluk, Robert G.
 APPLICANT: Mackenzie, Alexander E.
 APPLICANT: Baird, Stephen
 TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/511,485
 FILING DATE: 04-AUG-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 07540/002001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-3070
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2540 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: DNA (genomic)
 US-08-511-185-3

Query Match 98.4%; Score 194.8; DB 4;
 Best Local Similarity 99.0%; Pred. No. 1.9e-60;
 Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TATGAAACGAGCTGGATTTTATGCTTAACTGGATAACAGGAGCTT 60
 Db 1461 TATGAAACGAGCTGGATTTTATGCTTAACTGGATAACAGGAGCTT 1520
 Qy 61 GCAGAGCTGGATTTTATGCTTAACTGGATAACAGGAGCTT 120
 Db 1521 GCAGAGCTGGATTTTATGCTTAACTGGATAACAGGAGCTT 1580
 Qy 121 GGAGGGCTCAGGATGGAACCCAAGTGAAACCCCTGGGACCATGCTAATGTGCTAC 180
 Db 1581 GGAGGGCTCAGGATGGAACCCAAGTGAAACCCCTGGGACCATGCTAATGTGCTAC 1640
 Qy 181 CCAGGGTGCATAATACCTA 198
 Db 1641 CCAGGTGCAATAACCTA 1658

RESULT 5
 US-09-239-867-3
 Sequence 3 Application US/09239867
 Patent No. 6331412
 GENERAL INFORMATION:
 APPLICANT: Robert G. Korneluk et al.
 TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
 TITLE OF INVENTION: MALE FERTILITY
 FILE REFERENCE: 07891/018002
 CURRENT APPLICATION NUMBER: US/09/219,867
 CURRENT FILING DATE: 1999-01-29
 PRIOR APPLICATION NUMBER: 60,073,001
 PRIOR FILING DATE: 1998-01-29
 NUMBER OF SEQ ID NOS: 10
 SEQ ID NO 3 Application US/09239867
 LENGTH: 1588
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-239-867-3

Query Match 87.4%; Score 173; DB 4;
 Best Local Similarity 92.4%; Pred. No. 1.1e-52;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TATGAAACGAGCTGGATTTTATGCTTAACTGGATAACAGGAGCTT 60
 Db 826 TATGAAACGAGCTGGATTTTATGCTTAACTGGATAACAGGAGCTT 60
 Qy 61 GCAAGAGCTGGATTTTATGCTTAACTGGATAACAGGAGCTT 120
 Db 886 GCAAGAGCTGGATTTTATGCTTAACTGGATAACAGGAGCTT 945
 Qy 121 GGAGGGCTCAGGATGGAACCCAAGTGAAACCCCTGGGACCATGCTAATGTGCTAC 180
 Db 946 GGAGGGCTCAGGATGGAACCCAAGTGAAACCCCTGGGACCATGCTAATGTGCTAC 1005
 Qy 181 CCAGGGTGCATAATACCTA 197

Db 1006 |||||||CCAGGGTCAAAATATCT 1022 ; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (4623)...(4623)
; OTHER INFORMATION: n can be any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (4622)...(4622)
; OTHER INFORMATION: n can be any nucleotide
; SEQ ID NO: 1
; NUMBER OF SEQ ID NOS: 47
; CURRENT APPLICATION NUMBER: US/09/392,580
; CURRENT FILING DATE: 1999-09-09
; SEQ ID NO: 1
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION
; FILE REFERENCE: RIS-0072
; CURRENT APPLICATION NUMBER: US/09/392,580
; CURRENT FILING DATE: 1999-09-09
; SEQ ID NO: 1
; NUMBER OF SEQ ID NOS: 47
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(1527)
; US-09-392-580-1
Query Match 87.4%; Score 173; DB 3; Length 5232;
Best Local Similarity 92.4%; Pred. No. 1.9e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Db 826 TATGAAGCAGGATCTACTTTGGAAACATGGATAATCTCAGTTAACAGGGACGAGCTT 60
Qy 1 TATGAAGCAGGATCTACTTTGGAAACATGGATAATCTCAGTTAACAGGGACGAGCTT 60
Db 886 GCAGAGCTGGATTTAGTCAGGTAAAGTGCGCTTCCACTCTGGA 120
Qy 61 GCAGAGCTGGATTTAGTCAGGTAAAGTGCGCTTCCACTCTGGA 120
Db 946 GGAGGGTCAACGGATTGGAGCCAAGTGAGACCCCTGGACCAGCANGCTAATGCPAC 180
Qy 121 GGAGGGTCAACGGATTGGAGCCAAGTGAGACCCCTGGACCAGCANGCTAATGCPAC 180
Db 1006 CCAGGGTCAAAATCT 1005
Query Match 87.4%; Score 173; DB 3; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.3e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Db 826 TATGAAGCAGGATCTACTTTGGAAACATGGATAATCTCAGTTAACAGGGACGAGCTT 885
Qy 61 GCAGAGCTGGATTATGGTTAGGTGAAGGGATAAAAGTGAGTCAGTTCACGTGGA 120
Db 886 GCAGAGCTGGATTATGGTTAGGTGAAGGTGATAAAAGTGAGTCAGTTCACGTGGA 945
Qy 121 GAAGGGCTACGGATTGGAGCCAGTGAGACCCCTGGACCAGCANGCTAATGCPAC 180
Db 946 GAAGGGCTACGTGAGACCCAGTGAGACCCCTGGGAACAACTGCTAAATGGTAT 1005
Qy 181 CCAGGGTCAAAATCT 197
Db 1006 CCAGGGTCAAAATCT 1022
RESULT 9
US-08-800-929A-3
; Sequence 3, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ FOR Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker Brady, Kristina
; REGISTRATION NUMBER:
; SEQ ID NO: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO: 3

REFERENCE/DOCKET NUMBER: 07891/009001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-428-0200

TELEX: 617-428-7045

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 5332 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: Other

LOCATION: 1..5232

OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.

US-08-800-929A-3

Query Match Score 173; DB 4; Length 5332;
 Best Local Similarity 92.4%; Pred. No. 1.9e-52;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TATGAAACCGGATCGTACTTTGGACATGGATACTCAGTTAACAGGAGCAGCTT 60
 Db 826 TATGAAACCGGATCTTACTTTGGACATGGATACTCAGTTAACAGGAGCAGCTT 885

Qy 61 GCAAGAGCTGGATTATGCTTAGGTGAAGCGATAAGTGAGTCCTTCACIGTGA 120
 Db 886 GCAAGAGCTGGATTATGCTTAGGTGAAGCGATAAGTGAGTCCTTCACIGTGA 945

Qy 121 GGAGGGTCACTGGATGAAAGCCCTGGGACCAGCATGTAAGTGAGTCCTTCACIGTGA 180
 Db 946 GGAGGGTCACTGGATGAAAGCCCTGGGACCAGCATGTAAGTGAGTCCTTCACIGTGA 1005

Qy 181 CCAGGGTGCATAATACCT 197
 Db 1006 CCAGGGTGCATAATACCT 1022

RESULT 10
 US-09-617-053A-3
 ; Sequence 3, Application US/09617053A
 ; Patent No. 6300492
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Tsang, Benjamin K.
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; FILE REFERENCE: 07891/009003
 ; CURRENT APPLICATION NUMBER: US/09/617,053A
 ; CURRENT FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 1997-02-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 5332
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-09-617-053A-3
 ; Sequence 3, Application US/09617053A
 ; Patent No. 6300492
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Tsang, Benjamin K.
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; FILE REFERENCE: 07891/009003
 ; CURRENT APPLICATION NUMBER: US/09/617,053A
 ; CURRENT FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 1997-02-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 5332
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-09-617-053A-3
 ; Sequence 3, Application US/09617053A
 ; Patent No. 6300492
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Tsang, Benjamin K.
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; FILE REFERENCE: 07891/009003
 ; CURRENT APPLICATION NUMBER: US/09/617,053A
 ; CURRENT FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 1997-02-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 5332
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-09-617-053A-3
 ; Sequence 3, Application US/09617053A
 ; Patent No. 6300492
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Tsang, Benjamin K.
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; FILE REFERENCE: 07891/009003
 ; CURRENT APPLICATION NUMBER: US/09/617,053A
 ; CURRENT FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 1997-02-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 5332
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-09-617-053A-3
 ; Sequence 3, Application US/09617053A
 ; Patent No. 6300492
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Tsang, Benjamin K.
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; FILE REFERENCE: 07891/009003
 ; CURRENT APPLICATION NUMBER: US/09/617,053A
 ; CURRENT FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 1997-02-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 5332
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-09-617-053A-3
 ; Sequence 3, Application US/09617053A
 ; Patent No. 6300492
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Tsang, Benjamin K.
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; FILE REFERENCE: 07891/009003
 ; CURRENT APPLICATION NUMBER: US/09/617,053A
 ; CURRENT FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 1997-02-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 5332
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-09-617-053A-3
 ; Sequence 3, Application US/09617053A
 ; Patent No. 6300492
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Tsang, Benjamin K.
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; FILE REFERENCE: 07891/009003
 ; CURRENT APPLICATION NUMBER: US/09/617,053A
 ; CURRENT FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 1997-02-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 5332
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-09-617-053A-3
 ; Sequence 3, Application US/09617053A
 ; Patent No. 6300492
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Tsang, Benjamin K.
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; FILE REFERENCE: 07891/009003
 ; CURRENT APPLICATION NUMBER: US/09/617,053A
 ; CURRENT FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 1997-02-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 5332
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

Query Match Score 87.4%; DB 4; Length 5332;
 Best Local Similarity 92.4%; Pred. No. 1.9e-52;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TATGAAACCGGATCGTACTTTGGACATGGATACTCAGTTAACAGGAGCAGCTT 60
 Db 826 TATGAAACCGGATCTTACTTTGGACATGGATACTCAGTTAACAGGAGCAGCTT 885

Qy 61 GCAAGAGCTGGATTATGCTTAGGTGAAGCGATAAGTGAGTCCTTCACIGTGA 120
 Db 886 GCAAGAGCTGGATTATGCTTAGGTGAAGCGATAAGTGAGTCCTTCACIGTGA 945

Qy 121 GGAGGGTCACTGGATGAAAGCCCTGGGACCAGCATGTAAGTGAGTCCTTCACIGTGA 180
 Db 946 GGAGGGTCACTGGATGAAAGCCCTGGGACCAGCATGTAAGTGAGTCCTTCACIGTGA 1005

Qy 181 CCAGGGTGCATAATACCT 197
 Db 1006 CCAGGGTGCATAATACCT 1022

RESULT 11
 US-09-121-979-3

Sequence 3, Application US/09121979
 ; Patent No. 6171821
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Holcik, Martin
 ; APPLICANT: Liston, Peter
 ; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
 ; FILE REFERENCE: 07891/021001
 ; CURRENT APPLICATION NUMBER: US/09/121,979
 ; CURRENT FILING DATE: 1998-07-24
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 711
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-09-121-979-3

Query Match Score 147.4%; DB 3; Length 711;
 Best Local Similarity 84.3%; Pred. No. 1.2e-43;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATGAGCAGGGATGTTACTTTGGACATGGATACTCAGTTAACAGGAGCAGCTT 71
 Db 10 TATGAGCAGGGCTTACTTTGGACATGGATACTCAGTTAACAGGAGCAGCTT 69

Qy 61 GCAAGAGCTGGATTATGCTTAGGTGAAGCGATAAGTGAGTCCTTCACIGTGA 120
 Db 70 GCAAGAGCTGGATTATGCTTAGGTGAAGCGATAAGTGAGTCCTTCACIGTGA 129

Qy 121 GGAGGGTCACTGGATGAAAGCCCTGGGACCAGCATGTAAGTGAGTCCTTCACIGTGA 180
 Db 130 GGAGGGTCACTGGATGAAAGCCCTGGGACCAGCATGTAAGTGAGTCCTTCACIGTGA 189

Qy 181 CCAGGGTGCATAATACCT 197
 Db 190 CCAGGGTGCATAATACCT 206

RESULT 12
 US-09-332-319-3

Sequence 3, Application US/09332319
 ; Patent No. 6171821
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Holcik, Martin
 ; APPLICANT: Liston, Peter
 ; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
 ; FILE REFERENCE: 07891/021002
 ; CURRENT APPLICATION NUMBER: US/09/332,319

CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: 09/121,979
; EARLIER FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 3
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-332-319-3

Query Match 13 Score 147.4; DB 4; Length 711;
Best Local Similarity 84.3%; Pred. No. 1.2e-43; Indels 0; Gaps 0;
Matches 166; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1 TATGAAAGCAGGATCGTACTTTGGACATGGATACTCAGTTAACAGGAGCAGCTT 60
Db 1.0 TATGAAAGCAGGATCGTACTTTGGACATGGATACTCAGTTAACAGGAGCAGCTT 69
Qy 61 GCAAGAGCTGGATTATGCCATTAGCTTAGGTGAAAGCGATTAAGTGAAAGTGCTTCACTGTGGA 120
Db 70 GCAGAGCTGGATTATGCCATTAGCTTAGGTGAAAGCGATTAAGTGCTTCACTGTGGA 129
Qy 121 GGAGGGCTCACCGATGGAACTGAAACCCATGGACCACCATGCTAACGTCTAC 180
Db 130 GGGGGCTAACGCCAACCTGGAACTGAAACCCAAAGGAGATCCCTGGGAAACROCATGCTAATGGTAT 189
Qy 181 CCAGGGTGCATAATACCT 197
Db 190 CCAGGTGCAATAATCT 206

RESULT 13 US-09-239-867-1
; Sequence 1; Application US/09239867
; Patent No. 631412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 1559
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1559)
; OTHER INFORMATION: n = A,T,C or G

Qy 1 TATGAAAGCAGGATCGTACTTTGGACATGGATACTCAGTTAACAGGAGCAGCTT 60
Db 800 TATGAAAGCAGGATCGTACTTTGGACATGGATACTCAGTTAACAGGAGCAGCTT 859
Qy 61 GCAAGAGCTGGATTATGCCATTAGCTTAGGTGAAAGCGATTAAGTGCTTCACTGTGGA 120
Db 860 GCAAGAGCTGGATTATGCCATTAGCTTAGGTGAAAGCGATTAAGTGCTTCACTGTGGA 919
Qy 121 GGAGGGCTCACGGATGGAACTGAAACCCATGGGACACATGCTAACGTCTAC 180
Db 920 GGAGGGCTAGCCAACTGAAAGCCAGGAATCCCTGGGAAACAGCATGCTAACATGCTAATGGTAT 979

Query Match 14 Score 147.4; DB 4; Length 1559;
Best Local Similarity 80.3%; Pred. No. 1.8e-43; Indels 0; Gaps 0;
Matches 166; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 181 CCAGGGTGCATAATACCT 197
Db 3119 CCAGGTGCAATAATCT 3103

RESULT 14 US-09-128-155-16/C
; Sequence 16; Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 18
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(152331)
; OTHER INFORMATION: n = A,T,C or G

Qy 1 TATGAAAGCAGGATCGTACTTTGGACATGGATACTCAGTTAACAGGAGCAGCTT 60
Db 3238 TAAGAGCTGGATTATGCCATTAGCTTAGGTGAAAGCGATTAAGTGCTTCACTGTGGA 120
Qy 61 GCAAGAGCTGGATTATGCCATTAGCTTAGGTGAAAGCGATTAAGTGCTTCACTGTGGA 120
Db 3238 TAAGAGCTGGATTATGCCATTAGCTTAGGTGAAAGCGATTAAGTGCTTCACTGTGGA 3179
Qy 121 GGAGGGCTCACGGATGGAACTGAAACCCATGGGACACATGCTAACGTCTAC 180
Db 3178 GGGGGCTAACGTGGAAACCCACCGAA-AACCTTGGGACACATATAATGGGAT 3120
Qy 181 CCAGGGTGCATAATACCT 197
Db 3115 CCAGGTGCAATAATCT 3103

RESULT 15 US-09-128-155-17
; Sequence 17; Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 17
; LENGTH: 176373
; TYPE: DNA

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2003, 02:27:21 ; Search time 66 Seconds

(without alignments)
 3013.686 Million cell updates/sec

Title: US-09-654-743-51
 Perfect score: 198
 Sequence: 1 tatgaagcaggatcgttac.....accagggtgcaataacta 198

Scoring table: IDENTITY_NUC
 Gapop 10.0 ; Gapext 1.0

Searched: 639749 seqs, 502280978 residues

Total number of hits satisfying chosen parameters: 1279498
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications NA:
 1: /cgn2_6/picodeata/1/pubpna/US07_PUBCOMB.seq:*
 2: /cgn2_6/picodeata/1/pubpna/PCT_1_NEW_PUB.seq:*
 3: /cgn2_6/picodeata/1/pubpna/US06_NEW_PUB.seq:*
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 6: /cgn2_6/picodeata/1/pubpna/PCTUS_PUBCOMB.seq:*
 7: /cgn2_6/picodeata/1/pubpna/US08_NEW_PUB.seq:*
 8: /cgn2_6/picodeata/1/pubpna/US08_PUBCOMB.seq:*
 9: /cgn2_6/picodeata/1/pubpna/US09_NEW_PUB.seq:*
 10: /cgn2_6/picodeata/1/pubpna/US09_PUBCOMB.seq:*
 11: /cgn2_6/picodeata/1/pubpna/US10_NEW_PUB.seq:*
 12: /cgn2_6/picodeata/1/pubpna/US10_PUBCOMB.seq:*
 13: /cgn2_6/picodeata/1/pubpna/US60_NEW_PUB.seq:*
 14: /cgn2_6/picodeata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	198	100.0	2100	9 US-09-201-936-9
2	194.8	98.4	2691	10 US-09-974-532-9
3	173	87.4	2404	9 US-09-964-899-3
4	173	87.4	2540	9 US-09-201-936-3
5	173	87.4	523	10 US-09-974-532-3
c	6	134.4	67.9	15231 9 US-10-095-407-16
7	109.6	55.4	176313	9 US-10-095-407-17
8	76	38.4	2676	9 US-09-201-936-5
9	76	38.4	3076	9 US-09-201-936-16
10	76	38.4	3076	10 US-09-954-446-1635
11	76	38.4	6669	10 US-09-974-532-13
12	68	34.3	2450	9 US-09-201-936-39
13	68	34.3	2675	10 US-09-974-532-11
14	65.8	33.2	2580	9 US-09-201-936-7
15	65.8	33.2	3532	10 US-09-880-107-3354
16	65.8	33.2	3732	10 US-09-974-532-7
17	61	30.8	3151	10 US-09-974-532-13
18	59.4	30.0	2416	9 US-09-201-936-41
19	56.4	28.5	3773	9 US-10-041-859-1

Sequence 1, Appl1	45	22.7	5504	8 US-08-913-322-1
Sequence 21, Appl1	22	45	22.7	6124 8 US-08-913-322-21
Sequence 184, Appl1	23	45	22.7	6133 8 US-08-913-322-2
Sequence 2, Appl1	24	45	22.7	6228 8 US-08-913-322-23
Sequence 23, Appl1	25	39.8	20.1	2291 10 US-09-778-922A-21
Sequence 21, Appl1	c	34.8	17.6	240 9 US-09-796-692-3493
Sequence 3493, Appl1	c	27	33.2	16.8 240 9 US-09-796-692-6687
Sequence 6687, Appl1	c	28	31.2	15.8 2226 9 US-10-011-588A-6
Sequence 6, Appl1	c	29	30.6	15.5 2290 10 US-09-739-254-30
Sequence 30, Appl1	c	30	30.4	15.5 2000 9 US-09-842-3000
Sequence 3000, Appl1	c	31	29.2	14.7 1011 10 US-09-770-445-222
Sequence 222, Appl1	c	33	28.8	14.5 2255 9 US-09-938-842-1065
Sequence 1065, Appl1	c	34	28.4	14.3 1503841 9 US-09-946-807-1
Sequence 1, Appl1	c	35	28.4	14.3 1503841 10 US-09-795-568-1
Sequence 1, Appl1	c	36	28.4	14.3 1503841 10 US-09-795-666-1
Sequence 189, Appl1	c	37	27.8	14.0 3411 10 US-09-925-302-189
Sequence 3474, Appl1	c	38	27.8	14.0 19112 10 US-09-764-842-3474
Sequence 1, Appl1	c	39	27.6	13.9 2160 9 US-10-115-195-1
Sequence 1, Appl1	c	40	27.6	13.9 6911 9 US-10-170-528-1
Sequence 3, Appl1	c	41	27.6	13.9 197997 10 US-09-922-246-3
Sequence 243, Appl1	c	42	27.4	13.8 75899 10 US-09-854-883-243
Sequence 274, Appl1	c	43	27.2	13.7 698 10 US-09-770-149-273
Sequence 933, Appl1	c	44	27.2	13.7 766 10 US-09-770-445-933
Sequence 2950, Appl1	c	45	27.2	13.7 5031 10 US-09-764-877-2950

ALIGNMENTS

RESULT 1	US-09-201-936-9	SEQUENCE 9, Application US/09201936
		Publication No. US20020187946A1
		GENERAL INFORMATION:
		APPLICANT: Korneluk, Robert G.
		APPLICANT: Mackenzie, Alexander E.
		APPLICANT: Baird, Stephen
		APPLICANT: Liston, Peter
		TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS, PROBES, AND DETECTION METHODS
		FILE REFERENCE: 07891/003003
		CURRENT APPLICATION NUMBER: US/09/201,936
		CURRENT FILING DATE: 1998-12-01
		EARLIER APPLICATION NUMBER: 09/011,356
		EARLIER FILING DATE: 1998-02-04
		EARLIER APPLICATION NUMBER: PCT/IB96/01022
		EARLIER FILING DATE: 1996-08-05
		EARLIER APPLICATION NUMBER: 08/576,956
		EARLIER FILING DATE: 1995-12-22
		NUMBER OF SEQ ID NOS: 45
		SEQ ID NO 9
		LENGTH: 2100
		TYPE: DNA
		ORGANISM: <i>Mus musculus</i>
		US-09-201-936-9
		Query Match 100.0%; Score 198; DB 9; Length 2100;
		Best Local Similarity 100.0%; Pred. No. 2.5e-59; Indels 0; Gaps 0;
		SEQUENCE 18, Conservative 0; Mismatches 0;
		SEQUENCE 19, Gaps 0;
		SEQUENCE 20, Gaps 0;
		SEQUENCE 21, Gaps 0;
		SEQUENCE 22, Gaps 0;
		SEQUENCE 23, Gaps 0;
		SEQUENCE 24, Gaps 0;
		SEQUENCE 25, Gaps 0;
		SEQUENCE 26, Gaps 0;
		SEQUENCE 27, Gaps 0;
		SEQUENCE 28, Gaps 0;
		SEQUENCE 29, Gaps 0;
		SEQUENCE 30, Gaps 0;
		SEQUENCE 31, Gaps 0;
		SEQUENCE 32, Gaps 0;
		SEQUENCE 33, Gaps 0;
		SEQUENCE 34, Gaps 0;
		SEQUENCE 35, Gaps 0;
		SEQUENCE 36, Gaps 0;
		SEQUENCE 37, Gaps 0;
		SEQUENCE 38, Gaps 0;
		SEQUENCE 39, Gaps 0;
		SEQUENCE 40, Gaps 0;
		SEQUENCE 41, Gaps 0;
		SEQUENCE 42, Gaps 0;
		SEQUENCE 43, Gaps 0;
		SEQUENCE 44, Gaps 0;
		SEQUENCE 45, Gaps 0;
		SEQUENCE 46, Gaps 0;
		SEQUENCE 47, Gaps 0;
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		SEQUENCE 94, Gaps 0;
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		SEQUENCE 98, Gaps 0;
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		SEQUENCE 105, Gaps 0;
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		SEQUENCE 107, Gaps 0;
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		SEQUENCE 109, Gaps 0;
		SEQUENCE 110, Gaps 0;
		SEQUENCE 111, Gaps 0;
		SEQUENCE 112, Gaps 0;
		SEQUENCE 113, Gaps 0;
		SEQUENCE 114, Gaps 0;
		SEQUENCE 115, Gaps 0;
		SEQUENCE 116, Gaps 0;
		SEQUENCE 117, Gaps 0;
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		SEQUENCE 120, Gaps 0;
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		SEQUENCE 136, Gaps 0;
		SEQUENCE 137, Gaps 0;
		SEQUENCE 138, Gaps 0;
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		SEQUENCE 141, Gaps 0;
		SEQUENCE 142, Gaps 0;
		SEQUENCE 143, Gaps 0;
		SEQUENCE 144, Gaps 0;
		SEQUENCE 145, Gaps 0;
		SEQUENCE 146, Gaps 0;
		SEQUENCE 147, Gaps 0;
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		SEQUENCE 150, Gaps 0;
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		SEQUENCE 152, Gaps 0;
		SEQUENCE 153, Gaps 0;
		SEQUENCE 154, Gaps 0;
		SEQUENCE 155, Gaps 0;
		SEQUENCE 156, Gaps 0;
		SEQUENCE 157, Gaps 0;
		SEQUENCE 158, Gaps 0;
		SEQUENCE 159, Gaps 0;
		SEQUENCE 160, Gaps 0;
		SEQUENCE 161, Gaps 0;
		SEQUENCE 162, Gaps 0;
		SEQUENCE 163, Gaps 0;
		SEQUENCE 164, Gaps 0;
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		SEQUENCE 168, Gaps 0;
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		SEQUENCE 170, Gaps 0;
		SEQUENCE 171, Gaps 0;
		SEQUENCE 172, Gaps 0;
		SEQUENCE 173, Gaps 0;
		SEQUENCE 174, Gaps 0;
		SEQUENCE 175, Gaps 0;
		SEQUENCE 176, Gaps 0;
		SEQUENCE 177, Gaps 0;
		SEQUENCE 178, Gaps 0;
		SEQUENCE 179, Gaps 0;
		SEQUENCE 180, Gaps 0;
		SEQUENCE 181, Gaps 0;
		SEQUENCE 182, Gaps 0;
		SEQUENCE 183, Gaps 0;
		SEQUENCE 184, Gaps 0;
		SEQUENCE 185, Gaps 0;
		SEQUENCE 186, Gaps 0;
		SEQUENCE 187, Gaps 0;
		SEQUENCE 188, Gaps 0;
		SEQUENCE 189, Gaps 0;
		SEQUENCE 190, Gaps 0;
		SEQUENCE 191, Gaps 0;
		SEQUENCE 192, Gaps 0;
		SEQUENCE 193, Gaps 0;
		SEQUENCE 194, Gaps 0;
		SEQUENCE 195, Gaps 0;
		SEQUENCE 196, Gaps 0;
		SEQUENCE 197, Gaps 0;
		SEQUENCE 198, Gaps 0;
		SEQUENCE 199, Gaps 0;
		SEQUENCE 200, Gaps 0;

Qy 121 GGAGGGCTCACGGATGGAACCAAGTGAAGGACCCCTGGACCATGCTAAGTGCTAC 180
 Db 1036 GGAGGGCTCACGGATGGAACCAAGTGAAGGACCCCTGGACCATGCTAAGTGCTAC 1095

Oy 181 CCAGGGTGCAAATACTTA 198
 Db 1096 CCAGGGTGCAAATACTTA 1113

RESULT 2
 US-09-974-592-9
 ; Sequence 9, Application US/09974592
 ; Patent No. US20020120121A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G
 ; APPLICANT: MacKenzie, Alexander E
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Tsang, Benjamin K
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; FILE REFERENCE: 07891/009004
 ; CURRENT APPLICATION NUMBER: US/09/974,592
 ; PRIORITY FILING DATE: 2001-10-09
 ; PRIORITY APPLICATION NUMBER: US 09/617,053
 ; PRIORITY FILING DATE: 1997-02-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 9
 ; LENGTH: 2691
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-09-974-592-9

Query Match 98.4%; Score 194.8; DB 10; Length 2691;
 Best Local Similarity 99.0%; Pred. No. 3.7e-58;
 Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TATGAGGCACGGATCGTTACTTTGGAACATGGATACTCAGTTAACAGGAGCAGCTT 60
 Db 1461 TATGAGGCACGGATCGTTACTTTGGAACATGGACATCCTCACTGTTAACAGGAGCAGCTT 1520

Qy 61 GCAAGAGCTGGATTATTATGCTTTAGGTGAAGGGATAAACTGAAGTGAAGTCAGTCACGTGGAA 120
 Db 1521 GCAAGAGCTGGATTATTATGCTTTAGGTGAAGGGATAAACTGAAGTGAAGTCAGTCACGTGGAA 1580

Qy 121 GGAGGGTCACTGGATGGAACCAAGTGAAGGACCCCTGGACCATGCTAAGTGCTAC 180
 Db 1581 GGAGGGTCACTGGATGGAACCAAGTGAAGGACCCCTGGACCATGCTAAGTGCTAC 1640

Qy 181 CCAGGGTGCAAATACTTA 198
 Db 1641 CCAGGGTGCAAATACTTA 16558

RESULT 3
 US-09-654-899-38
 ; Sequence 38, Application US/09964899
 ; Patent No. US20020174446A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Dalia et al.
 ; TITLE OF INVENTION: Identification of Genes Involved in
 ; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
 ; FILE REFERENCE: 4-31612 A
 ; CURRENT FILING DATE: 2001-09-27
 ; PRIORITY APPLICATION NUMBER: 60/236,893
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIORITY APPLICATION NUMBER: 60/298,309

Query Match 87.4%; Score 173; DB 9; Length 2404;
 Best Local Similarity 92.4%; Pred. No. 1.6e-50;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TATGAGGCACGGATCGTTACTTTGGAACATGGATACTCAGTTAACAGGAGCAGCTT 60
 Db 827 TATGAGGCACGGATTTACTTTGGACATGGATACTCAGTTAACAGGAGCAGCTT 886

Qy 61 GCAAGAGCTGGATTATTATGCTTTAGGTGAAGGGATAAGTGAAGTCAGTCACGTGGAA 120
 Db 887 GCAGAGAGCTGGATTATTATGCTTTAGGTGAAGGGATAAGTGAAGTCACGTGGAA 946

Qy 121 GGAGGGTCACTGGATGGAACCCCTGGACCATGCTAACTGAAGTGAAGTCACGTGGAA 180
 Db 947 GGAGGGCTAACTGATTGGAAGGCCAGTGAAGACCCCTGGAAACACATGCTAAATGGTAA 1006

Qy 181 CCAGGGTGCAAATACTT 197
 Db 1007 CCAGGGTGCAAATACTT 1023

RESULT 4
 US-09-201-936-3
 ; Sequence 3, Application US/09201936
 ; Publication No. US20020187946A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: MacKenzie, Alexander E.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Feature, variation
 ; TITLE OF INVENTION: MAMMALIAN TAP GENE FAMILY, PRIMERS,
 ; PROBES, AND DETECTION METHODS
 ; FILE REFERENCE: 07891/003003
 ; CURRENT APPLICATION NUMBER: US/09/201,936
 ; EARLIER APPLICATION NUMBER: 09/011,356
 ; EARLIER FILING DATE: 1998-12-01
 ; EARLIER FILING DATE: 1998-02-04
 ; EARLIER APPLICATION NUMBER: PCT/IB96/01022
 ; EARLIER FILING DATE: 1996-08-05
 ; EARLIER APPLICATION NUMBER: 08/576,956
 ; EARLIER FILING DATE: 1995-12-22
 ; EARLIER APPLICATION NUMBER: 08/511,485
 ; EARLIER FILING DATE: 1995-08-04
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 3
 ; LENGTH: 2540
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE: variation
 ; NAME/KEY: variation
 ; LOCATION: (2540)..(2540)
 ; OTHER INFORMATION: N may be any nucleotide
 US-09-201-936-3

Qy 1 TATGAGGCACGGATCGTTACTTTGGAACATGGATACTCAGTTAACAGGAGCAGCTT 60
 Db 826 TATGAGGCACGGATTTACTTTGGACATGGATACTCAGTTAACAGGAGCAGCTT 885

Qy 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGGATAAACTGAAGTGAAGTCAGTCACGTGGAA 120

RESULT 5 - 1
 US-09-974-592-3
 Sequence 3, Application US/09974592
 Patent No. US2002120121A1
 GENERAL INFORMATION:
 APPLICANT: Korneluk, Robert G
 APPLICANT: Mackenzie, Alexander E
 APPLICANT: Liston, Peter
 APPLICANT: Baird, Stephen
 APPLICANT: Tsang, Benjamin K
 APPLICANT: Pratt, Christine
 TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE DISEASE
 FILE REFERENCE: 07891/009004
 CURRENT APPLICATION NUMBER: US/09/974,592
 CURRENT FILING DATE: 2001-10-09
 PRIOR APPLICATION NUMBER: US 09/617 , 053
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US 08/800 , 329
 PRIOR FILING DATE: 1997-02-13
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 5232
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE: variation
 NAME/KEY: variation
 LOCATION: 4623
 OTHER INFORMATION: n can be any nucleotide
 NAME/KEY: variation
 LOCATION: 4622
 OTHER INFORMATION: n can be any nucleotide
 OS-09-974-592-3

Query Match 1 TATGAGCACCGATCTTACTTTGGAAACATGGATAACATGGTAAAGTGCTAC 180
 Best Local Similarity 92.4%; Pred. No. 2.2e-50; Length 5232;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TATGAGCACCGATCTTACTTTGGAAACATGGATAACATGGTAAAGTGCTAC 60
 Db 945 GGAGGGCTTAACGTGTTAGCTTAACTGGAAACACATGCTAAATGGTAT 1005
 Qy 181 CCAGGGTGCATAATACCT 197
 Db 1006 CCAGGGTGCATAATACCT 1022

RESULT 5 - 1
 US-09-974-592-3
 Sequence 3, Application US/09974592
 Patent No. US2002120121A1
 GENERAL INFORMATION:
 APPLICANT: Pan, Yang
 TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
 FILE REFERENCE: 09404/052001
 CURRENT APPLICATION NUMBER: US/10/095,407
 CURRENT FILING DATE: 2002-03-11
 PRIOR APPLICATION NUMBER: US 60/091,650
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: US 60/054,646
 PRIOR FILING DATE: 1997-08-04
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 16
 LENGTH: 152331
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)...(152331)
 OTHER INFORMATION: n = A,T,C or G
 US-10-095-407-16

Query Match 1 TATGAGCACCGATCTTACTTTGGAAACATGGATAACATGGTAAAGTGCTAC 60
 Best Local Similarity 83.2%; Pred. No. 3.6e-16; Length 152331;
 Matches 164; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

Qy 61 GCAAGAGCTGGATTATTGGTTAGGTAAAGTGCTAAAGTGCTAAAGTGCTAC 120
 Db 3238 TCAAGAGCTGGATTATTGGTTAGGTAAAGTGCTAAAGTGCTAAAGTGCTAC 3179
 Qy 121 GGAGGGCTCAGGATTGGGAACGCAAGTGAAGAACCCCTGGGACCATGCTAAAGTGCTAC 180
 Db 3178 GGAGGGCTAAGTGGGAAACGGAAACACATAAAAGGGAT 3120

RESULT 7
 US-10-095-407-17
 Sequence 17, Application US/10095407
 Patent No. US2002164330A1
 GENERAL INFORMATION:
 APPLICANT: Pan, Yang
 TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
 FILE REFERENCE: 09404/052001
 CURRENT APPLICATION NUMBER: US/10/095,407
 CURRENT FILING DATE: 2002-03-11
 PRIOR APPLICATION NUMBER: US 60/091,650
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: US 60/054,646
 PRIOR FILING DATE: 1997-08-04
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: fastSEQ for Windows Version 3.0
 SEQ ID NO 17
 LENGTH: 176373
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)...(176373)
 OTHER INFORMATION: n = A,T,C or G
 US-10-095-407-17

Query Match 1 CCAGGGTGCATAATACCT 197
 Best Local Similarity 86.4%; Pred. No. 2e-27;

RESULT 6
 US-10-095-407-16/c
 Sequence 16, Application US/10095407
 Patent No. US2002164330A1

Matches 121; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 58 CTTGGCAAGAGCTGGATTTTATGCTTAGTGAAGCGATAAAAGTGAAGTGCCTCCACGT 117
Db 12549 CTTAAAGACTGGATTATGCTTAGTGAAGTGTAAAGTAAAGTAAAGTCACTGT 12608

RESULT 9
US-09-954-531-16
; Sequence 16, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954-531
; CURRENT FILING DATE: 2002-05-02
; PRIORITY NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIORITY NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIORITY NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIORITY NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIORITY NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 16
; LENGTH: 3076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-16

Query Match 38.4%; Score 76; DB 9; Length 3076;
Best Local Similarity 67.9%; Pred. No. 2e-16;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 118 GGAGGAGGGTCACGGATGGAAAGCCAAGTGAAACCCCTGGGACCAGATGTAAGTGC 177
Db 12609 GGAGGGGGTCACGTGGAAAGCCAGGGAAAGCCCTGGGACAACATGATAATGG 12668

RESULT 8
US-09-201-936-5
; Sequence 5, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows version 3.0
; SEQ ID NO: 5
; LENGTH: 2676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: variation
; NAME/KEY: variation
; LOCATION: (2470) .. (2470)
; OTHER INFORMATION: N may be any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2476) .. (2476)
; OTHER INFORMATION: N may be any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2483) .. (2483)
; OTHER INFORMATION: N may be any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2602) .. (2602)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-5

Query Match 38.4%; Score 76; DB 9; Length 2676;
Best Local Similarity 67.9%; Pred. No. 1.9e-16;
Matches 106; Conservative 50; Mismatches 0; Indels 0; Gaps 0;

Qy 42 AGTTAACAGGAGCCTGGAAAGCTGTGAAAGCTGTAGTGTAAAGT 101
Db 998 AGTTAACATCCGAGCTTGGAAAGTGGGTAAACGTGTGATGT 1057

RESULT 10
US-09-954-456-1635
; Sequence 1635, Application US/09954456
; Patent No. US/020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954-456
; CURRENT FILING DATE: 2001-09-18
; PRIORITY NUMBER: US/60/233,617
; PRIORITY NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIORITY NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIORITY NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIORITY NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIORITY NUMBER: US/60/235,638

PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 1635
; LENGTH: 3076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1635

Query Match 38.4%; Score 76; DB 10; Length 3076;
Best Local Similarity 67.9%; Pred. No. 2e-16;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 4 AGTTAACAGGAGCAGCTTCAGAGCTGGATTATGGTTAGGTGAAGCGATAAGT 101
Db 1534 AGTTAACCTGAGCAGCTGGCGTTTATTATGTGGTAAACAGTGATGAGT 1593

Qy 102 GAAGTGCTCCACCTGGAGGGGCTCACGGATGGAAAGCCAATGTGAAGCCCTGGGA 161
Db 1594 CTAATGCTTGGCTGATGGTGGACTCAAGTGTGGAAATCTGGAGTATCATGGG 1653

Qy 162 CCAGCATGCTTAAGGAGCTACCCAGGGTGCATAATCT 197
Db 1654 TCAACATGCCAAGCTGGTCCAAAGGTGTAGTACTT 1689

RESULT 11
US-09-974-592-5
; Sequence 5, Application US/09974592
; GENERAL INFORMATION:
; APPLICANT: Kornieluk, Robert G
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 5
; LENGTH: 6669
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: variation
; NAME/KEY: variation
; LOCATION: (367)....(951)
; OTHER INFORMATION: n can be any nucleotide

US-09-974-592-5

Query Match 38.4%; Score 76; DB 10; Length 6669;
Best Local Similarity 67.9%; Pred. No. 2.8e-16;
Matches 106; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

Qy 42 AGTTAACAGGAGCAGCTTCAGAGCTGGATTATGGTGAAGGCATAAGT 101
Db 5030 AGTTAACATCCPGAGCAGCTGGAGGGTTTATTATGGGTTAACAGTGATGT 5030

Qy 102 GAAGTGCTCCACCTGGAGGGCTCACGGATGGTTAGGTGAAGCGATAAGT 101
Db 5090 CAAATCTTGTGCTGATGTTGGATCTGGATGTCAGTGATGTCGGTGGATCTGGATGTCGGTGGATCTGGATGTCGGTGGATCTGGGGT 5149

Qy 162 CCAGCATGCTTAAGGAGCTACCCAGGGTGCATAATCT 197
Db 5150 TCAACATGCCAAGTGTCCAAAGGTGTAGTACTT 5185

RESULT 12
US-09-201-936-39
; Sequence 39, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Kornieluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 39
; LENGTH: 2450
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-39

Query Match 34.3%; Score 68; DB 9; Length 2450;
Best Local Similarity 64.7%; Pred. No. 1.2e-13;
Matches 101; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 42 AGTTAACAGGAGCAGCTGGAGGTGGTTAGGTGAAGCGATAAGT 101
Db 965 AGTTAACCTCCAGGAACCTGCAAGTGGGCTTTATAACAGAACAGTGATGT 1024

Qy 102 GAAGTGCTCCACCTGGAGGGCTCACGGATGGTTAGGTGAAGCGATAAGT 101
Db 1025 CAAGCTTATGCTGATGTTGGCTGAGTGGTGGATCTGGATGACCCGGGGT 1084

Qy 162 CCAGCATGCTTAAGGAGCTACCCAGGGTGCATAATCT 197
Db 1085 GGACATGCCAAGTGTCCAAAGGTGTAGTACTT 1120

RESULT 13
US-09-974-592-11
; Sequence 11, Application US/09974592
; Patent No. US2002012021A1
; GENERAL INFORMATION:
; APPLICANT: Kornieluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; DISEASE
; FILE REFERENCE: 07891/003004

CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIORITY NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIORITY NUMBER: US 08/800,929
; PRIORITY FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: fastSEQ for Windows Version 4.0
; SEQ ID NO: 11
; LENGTH: 2676
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-974-592-11

Query Match 34 3%; Score 68; DB 10; Length 2676;
Best Local Similarity 64.7%; Pred. No. 1.2e-13;
Matches 101; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 42 AGTTAACAGGAGCAGGTCTGCAAGCTGGATTTATGCTTAGGTAGGGATAAAGT 101
Db 1106 AGTCATCCGAACTGCAGTGCCTGGCTTTATATAAGGAAACAGTGATGTT 1165

Qy 102 GAATGCTTCCACTGTGAGGAGGCTGCAAGGATGGAAGCCAAGTGAAGCCNGGA 161
Db 1166 CAACTGTTTGTGTTGATGGCTGGCTGAGGCTGGAGATCTGGAGATGACCCCTGGGT 1225

Qy 162 CCACCATGGTAAAGTGTACCCAGGTGCAAAATACCT 197
Db 1226 GGAACATGCCAAGTGGTTCCAGGTGTGACTT 1261

RESULT 14
US-09-2011-936-7
; Sequence 7, Application US/09/2011-936-7
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/2011-936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/0111,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO: 7
; LENGTH: 2580
; SOFTWARE: FastSEQ for Windows Version 3.0
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2412)..(2412)
; OTHER INFORMATION: N may be any nucleotide
US-09-2011-936-7

Query Match 33 2%; Score 65.8; DB 9; Length 2580;
Best Local Similarity 60.2%; Pred. No. 7e-13;
Matches 109; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy 17 TTACTTTGGAAACATGGATACTGAGTAACAGGAGCAGCTTGCAAGAGGCGATT 76
Db 1064 TTATGACTGGCCATCTAGTGTCCAGTCAAGCTGAGCTGAGTGTGGTTTT 1123

Qy 77 ATGCTTAAAGTGAAGGGATAAAGTGAAGTGCCTTCAACTGTGAGGAGGCTACGGATT 76
Db 1124 ATTATGGGTCACATGGTCAATGTGATGTTGGTGTGATGTTGGTGTGTT 1183

Qy 137 GGAAAGCCAAAGTGAAGACCCCTGGACAGCAGTCAACTGTACCCAGGTGAAACC 196
Db 1184 GCGAATCTGGATGGTCATGGTAAACATGCCAAGTGGTTCCAGGTGTGACTTCT 1243

Qy 197 T 197
Db 1244 T 1244

RESULT 15
US-09-880-107-3354
; Sequence 3354, Application US/09880107
; Patent No. US20020429841
; GENERAL INFORMATION:
; APPLICANT: Horne, Darch T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SEQ ID NO: 3354
; LENGTH: 3532
; SOFTWARE: PatentIn Ver. 2.1
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 037547
US-09-880-107-3354

Query Match 33 2%; Score 65.8; DB 10; Length 3532;
Best Local Similarity 60.2%; Pred. No. 8.1e-13;
Matches 109; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy 17 TTACTTTGGAAACATGGATACTGAGTGCCTTCAACTGTGAGGAGGCTACGGATT 76
Db 1986 TTATGACTGGCCATCTAGTGTCCAGTCAAGCTGAGCTGAGTGTGGTTTT 2045

Qy 77 ATGCTTAAAGTGAAGGGATAAAGTGAAGTGCCTTCAACTGTGAGGAGGCTACGGATT 76
Db 2046 ATTATGGGTCACATGGTCAATGTGATGTTGGTGTGATGTTGGCTGAGGGTT 2105

Qy 137 GGAAAGCCAAAGTGAAGACCCCTGGACAGCAGTCAACTGTACCCAGGTGAAACC 196
Db 2106 GCGAATCTGGATGGTCATGGTAAACATGCCAAGTGGTTCCAGGTGTGACTTCT 2165

Qy 197 T 197
Db 2166 T 2166

Search completed: April 19, 2003, 03:05:22
Job time : 148 secs

GenCore version 5.1.4_p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2003, 01:38:31 ; Search time 10:57 Seconds

(without alignments)
3033.781 Million cell updates/secTitle: US-09-654-743-51
Perfect score: 198Scoring table: IDENTITY_NUC
GAPOP 10.0 , Gapext 1.0

Searched: 16154066 seeds, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listeing first 45 summaries
Database : EST:*

1: em_estba:*
 2: em_estbm:*
 3: em_estlin:*
 4: em_estmu:*
 5: em_estoy:*
 6: em_estpi:*
 7: em_estro:*
 8: em_htc:*
 9: gb_est1:*
 10: gb_htc:*
 11: gb_htc:*
 12: gb_est3:*
 13: gb_est4:*
 14: gb_est5:*
 15: em_estfun:*
 16: em_estom:*
 17: gb_gss:*
 18: em_gss_hum:*
 19: em_gss_inu:*
 20: em_gss_pln:*
 21: em_gss_vrt:*
 22: em_gss_fun:*
 23: em_gss_mam:*
 24: em_gss_mus:*
 25: em_gss_other:*
 26: em_gss_pro:*
 27: em_gss_lod:*

168 84.8 628 9 AI573382

108 54.5 617 10 BB663325

103.4 52.0 504 10 BB650856

100.8 50.9 318 12 BF659610

98 49.5 566 13 BM220130

98 49.5 584 14 BQ552032

168 84.8 628 9 AI573382

108 54.5 617 10 BB663325

103.4 52.0 504 10 BB650856

100.8 50.9 318 12 BF659610

98 49.5 566 13 BM220130

98 49.5 584 14 BQ552032

168 84.8 628 9 AI573382

108 54.5 617 10 BB663325

103.4 52.0 504 10 BB650856

100.8 50.9 318 12 BF659610

98 49.5 566 13 BM220130

98 49.5 584 14 BQ552032

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query	Match Length	DB ID	Description
c 1	168	84.8	628	9 AI573382	AI573382 mn8ej12.x
c 2	108	54.5	617	10 BB663325	BB663325 BB663325
c 3	103.4	52.0	504	10 BB650856	BB650856 BB650856
c 4	100.8	50.9	318	12 BF659610	BF659610 uzb8ej12.x
c 5	98	49.5	566	13 BM220130	BM220130 C0935E09.x
c 6	98	49.5	584	14 BQ552032	BQ552032 H4013A06-

ALIGNMENTS

RESULT 1

AI573382/c

LOCUS mRNA linear EST 16-APR-1999

DEFINITION mm8ej12.x1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:507023; similar to TR:060989 Q60989 MIHA .;

ACCESSION AA35707 EST63004

VERSION BM26304 1f0/e0.9.y

KEYWORDS EST

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murine; Mus.

REFERENCE I (bases 1 to 628)

AUTHORS Marra M., Hillier L., Kucaba T., Martin J., Beck C., Wylie T., Underwood R., Steptoe M., Theising B., Allen M., Bowers Y., Person B., Swaller T., Gibbons M., Pape D., Harvey N., Schutte R., Ritter E., Kohn S., Shin T., Jackson Y., Cardenas M., McCann R.

TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL Unpublished (1999)

COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNLN; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand

FEATURES	High quality sequence stop: 440.
source	Location/Qualifiers 1 .. 628 /organism="Mus musculus" /db_xref="Taxon:10090" /clone="IMAGE:550702" /clone.lib="Stratagene mouse Tcell" /tissue_type="Tcell" /dev_stage="M30 CD4+ cells" /lab_host="SOLR (kanamycin resistant)" /note="Organ: blood; Vector: plasmid SK-; Site_1: ECORI; Site_2: XbaI; Cloned unidirectionally. Primer: Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb; Uni-ZAP XR vector; -5' adapter sequence: 5'-GAATTCGCAGG 3' -3' adaptor sequence: 5'-CTCGAGTTTCTTCTTCTTCTT 3'*
BASE COUNT	163 a 115 g 211 t 2 others 8
ORIGIN	Query Match 84.8%; Score 168; DB 9; Length 628; Best Local Similarity 93.4%; Prd. No. 1.7e-43; Matches 185; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
FEATURES	source QY 1 TATGAAAGCACGGATCGTTACCTTGGAACATGGATACTACTAGTTAACAGGAGCAGCTT 60 Db 604 TATGAAAGCACGGATCGTTACCTTGGAACATGGACATCCGTCACTGTCAAAGGAGCAGCTT 545 QY 61 GGAAAGACTGTGATTATGCTTTAGTGTTAGGTGAAGSGATAAAGGTAAGTGAATGCTTCACTGTGGA 120 Db 544 GGAAAGACTGTGATTATGCTTTAGTGTTAGTGAAAGGCGTAAAGTGAAGTGTCTACTGTGGA 486 QY 121 GGAGGGCTCA CGGATGGAA GCGCAAGTGAAGAACCCCTGGGACCGATGCTTAAGTGTCTAC 180 Db 485 GGAGGGCTCA CGGATGGAA GCGCAAGTGAAGAACCCCTGGGACCGATGCTTAAGTGTCTAC 426 QY 181 CCAGGGTGC AATAACCTA 198 Db 425 NCAGGGTGC AATAACCTA 408
RESULT 2	BB663325 617 bp mRNA linear EST 26-OCT-2001 LOCUS BB663325 RIKEN full-length enriched, 15 days embryo head Mus DEFINITION muscleus cDNA clone D930039G22 5', mRNA sequence. ACCESSION BB663325 VERSION 1 KEYWORDS EST SOURCE ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus. REFERENCE Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda, M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,A., Saito,R., Sakai,C., Sano,H., Sasaki, D., Shibata,K., Shinanawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyoda,T., Muramatsu,M., and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001) Unpublished (2001)
TITLE	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-resgsc.riken.go.jp/ URL: http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh, M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to
JOURNAL	RESULTS 3 BB650856 LOCUS
COMMENT	504 bp mRNA linear EST 26-OCT-2001 BB650856 LOCUS

DEFINITION BB650856 RIKEN full-length enriched, 0 day neonate cerebellum Mus musculus cDNA clone C230036005 5', mRNA sequence.

ACCESSION BB650856

VERSION BB650856.1 GI:16485110

KEYWORDS EST.

ORGANISM house mouse.

MUS MUSCULUS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 504)

AUTHORS Arakawa, T., Hiramoto, K., Horii, F., Iishi, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, P., Sakai, R., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y.

TITLE RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

JOURNAL Unpublished (2001)

COMMENT Contact: Yoshihiko Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan FAX: 81-45-503-9222 Email: genome.res@gscc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/ Carninci, P., Shibata, Y., Hayatsu, N., Sugihara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuuwa, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771. (2000) Konno, H., Fukunishi, Y., Shibata, K., Y., and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kyosawa, H., Yamamoto, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., and Hayashizaki, Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

1. 504 /organism="Mus musculus" /db_xref="taxon:10090" /clone="230036005" /clone_id="RIKEN full-length enriched, 0 day neonate cerebellum" /tissue_type="cerebellum" /dev_stage="0 day neonate" /lab_host="DHIOB" /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGGATCCAGAGCTTCTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by

cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 479.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GACAGAGATTCATCGACTTAATTAACTCCCCCCCC 3']. cDNA was cleaved with XbaI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC 1."

BASE COUNT	ORIGIN	BASE COUNT	ORIGIN
126 a	Mus musculus	128 c	Mus musculus
98 t	1 others	98 t	1 others
Query Match	Score 103.4; DB 10; Length 504;	Query Match	Score 103.4; DB 10; Length 504;
Best Local Similarity	93.9%; Prod. No. 1.3e-22;	Best Local Similarity	93.9%; Prod. No. 1.3e-22;
Matches	107; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	Matches	107; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy	85 GGTGAAGGGATAAAGTGAACTGCTTCCACGTGGAGGGCTACGGATGGAGGCCA 144	Qy	85 GGTGAAGGGATAAAGTGAACTGCTTCCACGTGGAGGGCTACGGATGGAGGCCA 144
Db	207 GGNGAAGCGATAAAGTGAACTGCTTCACTGGAGGGCTACGGATGGAGGCCA 266	Db	207 GGNGAAGCGATAAAGTGAACTGCTTCACTGGAGGGCTACGGATGGAGGCCA 266
Qy	145 AGTGAAGACCCCTGGGACGAGCATGTAAGTGCTACCGGTGAAATACTTA 198	Qy	145 AGTGAAGACCCCTGGGACGAGCATGTAAGTGCTACCGGTGAAATACTTA 198
Db	267 AGTGAAGACCCCTGGGACGAGCATGTAAGTGCTACCGGTGAAATACTTA 320	Db	267 AGTGAAGACCCCTGGGACGAGCATGTAAGTGCTACCGGTGAAATACTTA 320

RESULT 4

BF659610/c

LOCUS BF659610

DEFINITION u288512.x1 NCI CGAP Lu29 Mus musculus mRNA similar to SW: TAP3_MOUSE Q60989 INHIBITOR OF APOPTOSIS PROTEIN 3 , mRNA sequence.

ACCESSION BF659610

VERSION BF659610.1 GI:11924744

KEYWORDS EST.

ORGANISM Mus musculus

SOURCE Mammalia; Eutheria; Rodentia; Chordata; Vertebrata; Euteleostomi; Murinae; Mus.

REFERENCE 1 (bases 1 to 318)

AUTHORS NCBI CGAP http://www.ncbi.nlm.nih.gov/nlmcgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D. Email: cgaps@remall.nih.gov

TISSUE Tissue Procurement: Gilbert Smith, Ph.D.

CNA DNA Library Preparation: Life Technologies, Inc.

CNA DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium at: image.lnl.gov/Image/html/irresources.shtml

MG:1436542 Possible reversed clone: polyT not found

Seq_Primer: 40UP from Gibco

High quality sequence stop: 226.

Location/Qualifiers

1. 318 /organism="Mus musculus"

FEATURES

source

1. 318 /strain="Mus musculus"

/strain "CZECH II"

/db_xref "taxon:10090"

/clone "IMAGE:13676174"

/clone lib "NCI CGAP Lu29"

/tissue-type "spontaneous tumor, metastatic to mammary stem cell origin."

/lab host "DHIOB"

/note "Organ: lung; Vector: PCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies, Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT

ORIGIN

Query Match 50.9%; Score 100.8; DB 12; Length 318;

Best Local Similarity	93.8%	Pred. No.	6.7e-22;
Matches	105; Conservative	0; Mismatches	7; Indels 0; Gaps 0;
ORIGIN	BASE COUNT	183 a	by Yulan Piao (NIA)."
QY 53 AGAGCTGCAAGAGCCTGGATTTAGTGTAGGGCCATAAGTGAGTGCCTCC 112	Query Match	4.95%	Score 98; DB 13; Length 566;
DB 317 AGAGCTGCAAGAGCCTGGATTTAGTGTAGGGCCATAAGTGAGTGCCTCC 258	Best Local Similarity	95.3%; Pred. No. 7.9e-21;	Gaps 0;
QY 113 ACTGTGGAGGGCTACGGATGGAGCCAAAGTGAAGACCCCTGGGACCA 164	Matches 101; Conservative	0; Mismatches 5; Indels 0; Gaps 0;	
DB 257 ACTGTGGAGGGCTACGGATGGAGCCAAAGTGAAGACCCCTGGGACCA 206	QY 82 TTAGGTGAAGGCCATAAAGTGAAAGTGTAGCTGGAGGGCTACGGATGGGAG 141		
QY 142 CCAAGTGAAGAACCCCTGGGACAGCATGCTAAGTGACCCAGGT 187	DB 260 TTAGGTGAAGGCCATAAAGTGAAAGTGTAGCTGGAGGGCTACGGATGGGAG 201		
QY 200 CCAAGTGAAGAACCCCTGGGACAGCATGCTAAGTGACCCAGGT 155	EST 20-JUN-2002		
RESULT 5	LOCUS	BQ552032	584 bp mRNA linear EST
BM220130/c	DEFINITION	H401A06_3	NIA Mouse 7.4K cDNA Clone Set
BM220130 LOCUS	ORGANISM	H401A06_3', mRNA sequence.	Mus musculus
C0935E08-3 NIA Mouse 12.5-dpc Male Genital Ridge/mesonephros cDNA Library (Long) Mus musculus cDNA clone C0935E08 3', mRNA sequence.	KEYWORDS	ACCESSION	BQ552032
BM220130	VERSION	VERSION	EST.
BM220130.1 GI:17780130	COMMENT	KWYWORDS	EST.
RESULTS	SOURCE	SOURCE	house mouse.
Mus musculus	ORGANISM	Mus musculus	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Fukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	REFERENCE	REFERENCE	1 (bases 1 to 584)
1 (bases 1 to 566)	AUTHORS	AUTHORS	VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., Martin,P.R., Stagg,C.A., Bassey,U., Aiba,K., Hamatani,T., Kargul,G.J., Luo,A.G. and Ko,M.S.H.
Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Pantano,S., Luo,A. and Ko,M.S.H.	TITLE	TITLE	Assembly, verification, and initial annotation of NIA 7.4K mouse cDNA clone set
Systematic Analyses of NIA Mouse 12.5-dpc Male Genital Ridge/mesonephros cDNA Library (Long)	JOURNAL	JOURNAL	Unpublished (2001)
Unpublished (2001)	COMMENT	COMMENT	Other ESTs: H4013A06-5
Contact: Dawood B. Dudekula	ORGANISM	CONTACT	Contact: Yong Qian
Laboratory of Genetics	KEYWORDS	ORGANISM	National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health	VERSION	KEYWORDS	333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA	COMMENT	COMMENT	Email: cdna@igsun.grc.nia.nih.gov
Email: cdna@igsun.grc.nia.nih.gov	FEATURES	FEATURES	This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7.4k.html for details.
Plate: C0935 Row: E column: 08	source	source	Plate: H4013 Row: A column: 06
Seq. Primer: -21M13 Forward	QUALIFIERS	QUALIFIERS	Seq. Primer: -21M13 Forward
High Quality sequence stop: 566	POLY-A	POLY-A	High Quality sequence stop: 584
POLY-A:Yes	LOCATION	LOCATION	POLY-A:Yes
Location/Qualifiers	FEATURES	FEATURES	Location/Qualifiers
1..566	source	source	1..584
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/strain="C57BL/6J"	QUALIFIERS	QUALIFIERS	/strain="C57BL/6"
/db_xref="niaeEST:H4013A06-3"	QUALIFIERS	QUALIFIERS	/db_xref="niaeEST:H4013A06-3"
/db_xref="niaeEST:H4013A06"	QUALIFIERS	QUALIFIERS	/db_xref="niaeEST:H4013A06"
/taxon:10090	QUALIFIERS	QUALIFIERS	/taxon:10090
/clone=C0935E08	QUALIFIERS	QUALIFIERS	/clone.lib="NIA Mouse 7.4K cDNA Clone Set"
/clone.lib="NIA Mouse 12.5-dpc Male Genital Ridge/mesonephros cDNA Library (Long)"	QUALIFIERS	QUALIFIERS	/sex="mixed"
/sex="Male"	QUALIFIERS	QUALIFIERS	/dev_stage="mixed"
/tissue_type="Male genital ridge/mesonephros"	QUALIFIERS	QUALIFIERS	/lab_host="DH10B"
/dev_stage="12.5-dpc"	QUALIFIERS	QUALIFIERS	/note="vector: pSPORT1; Site_1: SalI; Site_2: NotI; This clone is among a rearrrayed set of 7,407 clones from more than 20 cDNA libraries."
/lab_host="DH10B"	QUALIFIERS	QUALIFIERS	Query Match 4.95%; Score 98; DB 14; Length 584;
NOTE: Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1533-1538 (2001). [PMID: 11544189]). Double-stranded cDNAs were synthesized with an Oligo(dT) primer Invitrogen.	QUALIFIERS	QUALIFIERS	Best Local Similarity 95.3%; Pred. No. 8.1e-21; Gaps 0;
5'-pGACTAGCTAGTCGGCGGCCCTTCTTCTTCTT-3'] from 1.8 µg of total RNA, treated with T4 DNA Polymerase, and purified by ethanol precipitation. The cDNAs were ligated to Lone-linker 5'-Sal4- purifed by phenol/chloroform, and separated from free linkers by Centriflon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centriflon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI-NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.4 kb. The library was constructed	BASE COUNT	189 a	by Yulan Piao (NIA)."
QY 82 TTAGGTGAAGGCCATAAAGTGAAAGTGTAGCTGGAGGGCTACGGATGGGAG 141	EST 20-JUN-2002		
DB 260 TTAGGTGAAGGCCATAAAGTGAAAGTGTAGCTGGAGGGCTACGGATGGGAG 201			

QY	142	CCAACTGAGAACCCCTGGGACCAAGCATGTGTAAGTGTACCCAGGGT	187		Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db	200	CCAACTGAGAACCCCTGGGACCAAGCATGTGTAAGTGTACCCAGGGT	155		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
RESULT	7				REFERENCE	1 (bases 1 to 536)
DEFINITION	BMB05359	BB605359	1177 bp	mRNA linear	AUTHORS	Ota,T., Nishikawa,T., Suzuki,Y., Kawai,Y., Ishii,S., Saito,K., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
LOCUS	AGENCOURT_6499731	NIH_MGC_124	Homo sapiens	CDNA clone IMAGE:5728685	TITLE	HRI human cDNA project; NIH human cDNA project; (Ota,T., Nishikawa,T., Suzuki,Y., Kawai,Y., Nagai,T., Sugano,S., Isogai,T.)
JOURNAL					COMMENT	Unpublished (2000)
VERSION	1	BB605359.1	GI:19122192		CONTACT	Takao Isogai
KEYWORDS					GENOMICS LABORATORY	
ORGANISM					HELIX RESEARCH INSTITUTE	
SOURCE	Human.				1532-3 Yana, Kisarazu, Chiba 292-0812, Japan	
REFERENCE					TEL: 81-438-52-3975	
AUTHORS					FAX: 81-438-52-3986	
TITLE					EMAIL: genomics@ri.co.jp	
JOURNAL					RESEARCH INSTITUTE; CDNA LIBRARY CONSTRUCTION; DEPARTMENT OF VIROLOGY, INSTITUTE OF MEDICAL SCIENCE, UNIVERSITY OF TOKYO, AND HELIX RESEARCH INSTITUTE.	
COMMENT					LOCATION/QUALIFIERS	
FEATURES					1..536	
source					/organism="Homo sapiens"	
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					/clone=NT2RM1000921"	
					/clone_1lib="NT2RM1"	
					/cell-type="teratocarcinoma"	
					/cell-line="NT2"	
					/note="vector: pUC19FRL3; mRNA from uninduced NT2 neuronal precursor cells"	
BASE COUNT					precursor cells"	
ORIGIN					172 a 105 c 126 g 124 t 9 others	
FEATURES						
source					Query Match 45.6%; Score 90.2; DB 9; Length 536;	
					Best Local Similarity 86.7%; Pred. No. 2.6e-18;	
					Matches 98; Conservative 0; Misماatches 15; Indels 0;	
					Gaps 0;	
FEATURES					QY	85
source					GGTGAAGCGATAAAGTGAAAGTCAGTGCCTCAGGATGGCTCACGGATTGGAAAGCCA 144	
					/db_xref="IMAGE:5728685"	
					/clone_1lib="NT2RM124"	
					/tissue-type="hippocampus"	
					/lab_host="DHIB"	
					/note="Organ: brain; Vector: PCMV-SPORT6; Site_1: Ecorv (destroyed); Site_2: NotI; RNA source: male hippocampus, age 27. Library is Oligo-dT primed and directionally cloned (Ecorv site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."	
BASE COUNT					Db	99
ORIGIN					GGTGAAGGTGATAAAGTAAGTAAAGTGTCTTACTGGAGANGGCTAACAGTATGGAGGCC 158	
FEATURES					QY	145
source					AGTGAAGGCCCTGGGACAGCATGCTTAAGTGTACCCAGGGGCAAACTCT 197	
					/db_xref="IMAGE:5728685"	
					/clone_1lib="NT2RM124"	
					/tissue-type="hippocampus"	
					/lab_host="DHIB"	
					/note="Organ: brain; Vector: PCMV-SPORT6; Site_1: Ecorv (destroyed); Site_2: NotI; RNA source: male hippocampus, age 27. Library is Oligo-dT primed and directionally cloned (Ecorv site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."	
BASE COUNT					Db	159
ORIGIN					AGTGAANACCTTGGGAAACACATGCTAAATGGTATCCAGGGTGCCTAAATATCT 211	
FEATURES					RESULT 9	
source					AV7066807	
					LOCUS AV7066807 ADB Homo sapiens mRNA linear EST 09-OCT-20000	
					DEFINITION AV7066807 ADB Homo sapiens cDNA clone ADCCOF01 5', mRNA sequence.	
					VERSION AV7066807.1 GI:10724085	
					KEYWORDS EST	
					ORGANISM Homo sapiens	
					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
					REFERENCE 1 (bases 1 to 716)	
					AUTHORS Peng, Y., Song, H., Huang, Q., Gu, Y., Gao, G., Xiao H., Xu, X., Li, N., Qian, B., Liu, F., Gu, W., Tu, Y., Jia, J., Cheng, Z., Xu, Z., Zeng, L., Hu, R., Cheo, J., Chen, Z., and Hao, Z.	
					JOURNAL	
					COMMENT Unpublished (2000)	
					CONTACT: Zequang Han	
					Chinese National Human Genome Center at Shanghai	
					351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai	
					201203, P. R. China	
					TEL: 86-21-580801919 (ex.45)	
					FAX: 86-21-580801922	
					EMAIL: hanzg@chgc.sh.cn	
					FEATURES This elnc is available at CHGC In Shanghai	
					Location/Qualifiers	

source 1. .716 "Homo sapiens"
 /db_xref="taxon:9606."
 /clone="ADBCFOI."
 /clone_lib="ADB"
 /tissue_type="Adrenal gland"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /xhoi="XhoI"
 /pBluescript_sk("-"); site_1: ECORI; site_2:
 BASE COUNT 207 a 148 c 193 g 163 t 5 others
 ORIGIN |
 Query Match 42.5%; Score 84.2; DB 10; Length 716;
 Best Local Similarity 84.1%; Pred. No. 2.8e-16;
 Matches 95; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
 RESULT 1.1
 AW375594 LOCUS AW375594
 DEFINITION QVO-CPO179-300999-024-d06 mRNA saptiens cdNA, mRNA sequence.
 ACCESSION AW375594
 VERSION AW375594.1 GI:6880157
 KEYWORDS EST.
 SOURCE human
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 354)
 AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
 TITLE The PAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2701922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=QVO&t2=QVO&t1=0179-300999-024-d06&t=1999-09-30&t4=1>)
 Seq. primer: puc 18 forward
 High quality sequence start: 12
 High quality sequence stop: 354.
 FEATURES Location/Qualifiers
 1. .354 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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 /dev_stage="adult"
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 BASE COUNT 91 a 70 c 83 g 97 t
 ORIGIN |
 Query Match 38.4%; Score 76; DB 10; Length 354;
 Best Local Similarity 67.9%; Pred. No. 7.9e-14;
 Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 ACCESSION 42 AGTTAACAGGAGCAGCTGGATTTATGCTTAGGTGAAGCGATAAAGT 101
 DEFINITION QY-AAGTGTCTTCACTGTGGAGGGCTACGGATGGAAAGCCAAAGTGAGCTGGGA 161
 ACCESSION 93 AGTTAACCTGGAGCTGGATTTATGCTTAGGTGAAGCGATAAAGT 152
 DEFINITION QY-102 GAATGTCCTTCACTGTGGAGGGCTACGGATGGAAAGCCAAAGTGAGCTGGGA 161
 ACCESSION 153 CAAATGCTTTCGTMGATGTTGGACTAGTGATGATCATGGGT 212
 FEATURES Query Match

Qy	162	CCAGCATGCTAAGTGTACCCAGGGTCAAAATACCT 197	Db	247	TCAACATGCCAAGTGGTTCCAAGGTGACTT 282
Db	213	TCAACATGCCAAGTGGTTCCAAGGTGACTT 248	RESULT 13		
DEFINITION	AW846507	AW846507-000179-240300-175-h08	LOCUS	AW75599	531 bp mRNA linear
ACCESSION	QVO-CM0179-AW846507	CT0179	DEFINITION	QVO-CM0179-300999-024-g04	Homo sapiens cDNA, mRNA sequence.
VERSION	1	EST.	ACCESSION	AW75599	EST 04-FEBB-2000
KEYWORDS	AW846507.1	GI:7942024	VERSION	AW75599.1	EST.
SOURCE	human.		SOURCE		
ORGANISM	Homo sapiens		ORGANISM		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.		REFERENCE	1 (bases 1 to 531)	
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Naga, L.M.A., da Silva, W. Jr., Zago, M.A., Bordim, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.		AUTHORS	HCPG http://www.ludwig.org.br/ORESPBS.	
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		TITLE	The FAPESP/LICR Human Cancer Genome Project.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		JOURNAL	Unpublished (1999)	
MEDLINE	20202663		COMMENT	COMMENT	
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil.		CONTACT:	Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil.	
FEATURES	source		FEATURES	source	
source	1. 402 /organism="Homo sapiens" /db_xref="taxon:9606" /clone.lib="CT0179" /dev_stage="Adult" /note="Organ: colon; vector: puc18; Site_1: SmaI; Site_2: Smal; A mini-library was made by cloning products derived from ORESPBS PCR (U.S. Letters Patent application No. 196716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		source	1. 531 /organism="Homo sapiens" /db_xref="taxon:9606" /clone.lib="CT0179" /dev_stage="Adult" /note="Organ: colon; vector: puc18 forward primer: puc18 reverse primer: puc 18 forward High quality sequence start: 16 High quality sequence stop: 531.	
BASE COUNT	158 a 108 c 121 g 144 t		BASE COUNT	158 a 108 c 121 g 144 t	
ORIGIN			ORIGIN		
Query Match	38.4%	Score 76; DB 10; Length 531;	Query Match	38.4%	Score 76; DB 10; Length 531;
Best Local Similarity	67.9%	Pred. No. 1e-13; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity	67.9%	Pred. No. 1e-13; Mismatches 0; Indels 0; Gaps 0;
Matches 106; Conservative 0; MisMatches 50;			Matches 106; Conservative 0; MisMatches 50;		
FEATURES	source		FEATURES	source	
source	1. 402 /organism="Homo sapiens" /db_xref="taxon:9606" /clone.lib="CT0179" /dev_stage="Adult" /note="Organ: colon; vector: puc18; Site_1: SmaI; Site_2: Smal; A mini-library was made by cloning products derived from ORESPBS PCR (U.S. Letters Patent application No. 196716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		source	1. 402 /organism="Homo sapiens" /db_xref="taxon:9606" /clone.lib="CT0179" /dev_stage="Adult" /note="Organ: colon; vector: puc18 forward primer: puc18 reverse primer: puc 18 forward High quality sequence start: 16 High quality sequence stop: 531.	
BASE COUNT	117 a 81 c 90 g 114 t		BASE COUNT	117 a 81 c 90 g 114 t	
ORIGIN			ORIGIN		
Query Match	38.4%	Score 76; DB 10; Length 402;	Query Match	38.4%	Score 76; DB 10; Length 532;
Best Local Similarity	67.9%	Pred. No. 8.6e-14;	Best Local Similarity	67.9%	Pred. No. 1e-09; Mismatches 0; Indels 0; Gaps 0;
Matches 106; Conservative 0; MisMatches 50;			Matches 106; Conservative 0; MisMatches 50;		
FEATURES	source		FEATURES	source	
source	1. 402 AGTTAACAGGAGCAC-TGCAAGAGCTGGATTATTAGCTTAGGTGAAGCGATAAACT 101		source	1. 402 AGTTAACAGGAGCAC-TGCAAGAGCTGGATTATTAGCTTAGGTGAAGCGATAAACT 101	
Qy	102 AGGTGCTCCACTGTGGAGGGCTACGGATGGAAAGCCCTGGA 161		Qy	102 AGGTGCTCCACTGTGGAGGGCTACGGATGGAAAGCCCTGGA 161	
Db	187 CAAATGCTTGATGAGTGGACTCAGTGGTTTATCTGGTAACAGTGATGT 246		Db	199 CAAATGCTTGATGAGTGGACTCAGTGGTTTATCTGGTAACAGTGATGT 258	
Qy	162 CCAGCATGCCAAGTGGTTCCAGGTGAAATACCT 197		Qy	162 CCAGCATGCCAAGTGGTTCCAGGTGAAATACCT 197	
DEFINITION	AW846425		DEFINITION	AW846425	
ACCESSION	QVO-CM0179-070300-143-d09		ACCESSION	QVO-CM0179-070300-143-d09	
VERSION	AW846425.1		VERSION	AW846425.1	
KEYWORDS	EST.		KEYWORDS	EST.	



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Indexing Officer: DSANFORD - DEBRA SANFORD

Team: OIPEBackFileIndexing

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No.	Doccode	Number of pages
1	SRNT	7

Total number of pages: 7

Remarks:

Order of re-scan issued on